

Product datasheet for **SC305580**

FGF8 (NM_033163) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: FGF8 (NM_033163) Human Untagged Clone
Tag: Tag Free
Symbol: FGF8
Synonyms: AIGF; FGF-8; HBGF-8; HH6; KAL6
Mammalian Cell Selection: None
Vector: [pCMV6-XL5](#)
E. coli Selection: Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene sequence for NM_033163 edited
CGGAGCCGCGCCATGGGCAGCCCCGCTCCGCGCTGAGCTGCCTGCTGTTGCACTTGC
TGGTCTCTGCCTCCAAGCCCAGGAAGGCCCGGGCAGGGCCCTGCGCTGGGCAGGGAGC
TCGCTTCCCTGTTCCGGGCTGGCCGGGAGCCCCAGGGTGTCTCCAACAGGTAACGTTC
AGTCTCACCTAATTTTACACAGCATGTGAGGGAGCAGAGCCTGGTGACGGATCAGCTCA
GCCGCGCTCATCCGGACCTACCAACTCTACAGCCGACACAGCGGAAGCACGTGCAGG
TCCTGGCCAACAAGCGCATCAACGCCATGGCAGAGGACGGCGACCCCTTCGCAAAGCTCA
TCGTGGAGACGGACACCTTTGGAAGCAGAGTTCGAGTCCGAGGAGCCGAGACGGGCTCT
ACATCTGCATGAACAAGAAGGGGAAGCTGATCGCCAAGAGCAACGGCAAAGGCAAGGACT
GCGTCTTACGGAGATTGTGCTGGAGAACAACACACAGCGCTGCAGAATGCCAAGTACG
AGGGCTGGTACATGGCCTTCACCCGCAAGGGCCGCCCCGCAAGGGCTCCAAGACGCGGC
AGCACCAGCGTGAGGTCCACTTCATGAAGCGGCTGCCCGGGGCCACCACACCACCGAGC
AGAGCCTGCGCTTCGAGTTCCTCAACTACCCGCCCTTCACGCGCAGCCTGCGCGGAGCC
AGAGGACTTGGCCCCGAGCCCCGATAGGTGCTGCCTGGCCCTCCCCACAATGCCAGAC
CGCAGAGAGGCTCATCTGTAGGGCACCCAAAACCAAGCAAGATGAGCTGTGCGCTGCT
CTGCAGGCTGGGAGGTGCTGGGAGAGCCCTGGGTTCCGGTTGTTGATATTGTTTGTGT
TGGGTTTTGCTGCTTTTTTTTTTTTTTTTTTTT

Restriction Sites: Please inquire

ACCN: NM_033163

Insert Size: 930 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).



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OTI Annotation:	The ORF of this clone has been fully sequenced and found to be a perfect match to NM_033163.1.
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:	<ol style="list-style-type: none">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_033163.1 , NP_149353.1
RefSeq Size:	1107 bp
RefSeq ORF:	735 bp
Locus ID:	2253
UniProt ID:	P55075
Cytogenetics:	10q24.32
Protein Families:	Druggable Genome, Secreted Protein
Protein Pathways:	MAPK signaling pathway, Melanoma, Pathways in cancer, Regulation of actin cytoskeleton
Gene Summary:	<p>The protein encoded by this gene is a member of the fibroblast growth factor (FGF) family. FGF family members possess broad mitogenic and cell survival activities, and are involved in a variety of biological processes, including embryonic development, cell growth, morphogenesis, tissue repair, tumor growth and invasion. This protein is known to be a factor that supports androgen and anchorage independent growth of mammary tumor cells. Overexpression of this gene has been shown to increase tumor growth and angiogenesis. The adult expression of this gene is restricted to testes and ovaries. Temporal and spatial pattern of this gene expression suggests its function as an embryonic epithelial factor. Studies of the mouse and chick homologs revealed roles in midbrain and limb development, organogenesis, embryo gastrulation and left-right axis determination. The alternative splicing of this gene results in four transcript variants. [provided by RefSeq, Jul 2008]</p> <p>Transcript Variant: This variant (F) encodes the longest isoform (F). 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>