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Product datasheet for SC326169

FGFR2 (NM_001144919) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	FGFR2 (NM_001144919) Human Untagged Clone
Tag:	Tag Free
Symbol:	FGFR2
Synonyms:	BBDS; BEK; BFR-1; CD332; CEK3; CFD1; ECT1; JWS; K-SAM; KGFR; TK14; TK25
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)

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Fully Sequenced ORF:

>SC326169 representing NM_001144919.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

GTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTA
CCGAGGAGATCTGCCGCCGCGATCGCCGGCGCGCCC
ATGGTCAGCTGGGGTCGTTTCATCTGCCTGGTCGTGGTCACCATGGCAACCTTGTCCCTGGCCCGGCCC
TCCTTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAAGATGCCATCTCATCCGGAGATGATGAGGAT
GACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGAGCACCATACTGGACCAAC
ACAGAAAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCC
GGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATT
GGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGA
AATTATACCTGTGTAGTGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAG
CGATCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGAC
GTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAG
AACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTCAAGCACTCGGGGATAAATAGT
TCCAATGCAGAAGTGCTGGCTCTGTTCAATGTGACCGAGGCGGATGCTGGGGAATATATATGTAAGGTC
TCCAATTATATAGGGCAGGCCAACCAGTCTGCCTGGCTCACTGTCCTGCCAAAACAGCAAGCGCCTGGA
AGAGAAAAGGAGATTACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTA
ATCGCCTGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTCAGC
AGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACAGTTTCGGCTGAG
TCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACACGCCTCTCTTCAACGGCAGAC
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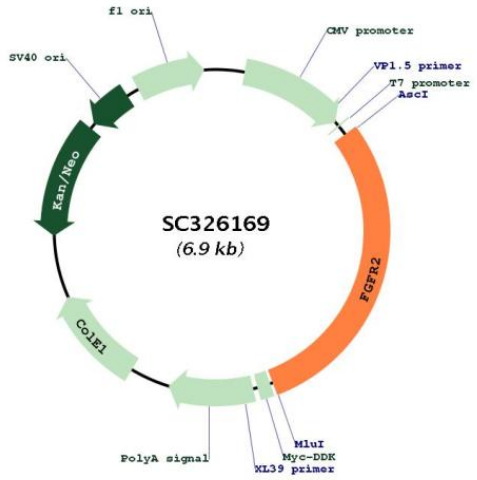
AATCTTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAAGGCAAC
CTCCGAGAATACCTCCGAGCCCGGAGGCCACCCGGGATGGAGTACTCCTATGACATTAACCGTGTTCCT
GAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAGCTGGCCAGAGGCATGGAGTACTTG
GCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTTGGTAACAGAAAACAATGTGATG
AAAATAGCAGACTTTGGACTCGCCAGAGATATCAACAATATAGACTATTACAAAAAGACCACCAATGGG
CGGCTTCCAGTCAAGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTC
TGGTCCTTCGGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCGTG
GAGGAACTTTTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCCAACTGCACCAACGAACTG
TACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACGTTCAAGCAGTTGGTAGAA
GACTTGGATCGAATTCTCACTCTCACAACCAATGAGATCTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites: AscI-MluI

Plasmid Map:



ACCN:	NM_001144919
Insert Size:	2043 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).
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.
RefSeq:	NM_001144919.1
RefSeq Size:	3011 bp
RefSeq ORF:	2043 bp
Locus ID:	2263
UniProt ID:	P21802
Cytogenetics:	10q26.13

Protein Families:	Druggable Genome, Protein Kinase, Secreted Protein, Transmembrane
Protein Pathways:	Endocytosis, MAPK signaling pathway, Pathways in cancer, Prostate cancer, Regulation of actin cytoskeleton
MW:	76.4 kDa
Gene Summary:	The protein encoded by this gene is a member of the fibroblast growth factor receptor family, where amino acid sequence is highly conserved between members and throughout evolution. FGFR family members differ from one another in their ligand affinities and tissue distribution. A full-length representative protein consists of an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member is a high-affinity receptor for acidic, basic and/or keratinocyte growth factor, depending on the isoform. Mutations in this gene are associated with Crouzon syndrome, Pfeiffer syndrome, Craniosynostosis, Apert syndrome, Jackson-Weiss syndrome, Beare-Stevenson cutis gyrata syndrome, Saethre-Chotzen syndrome, and syndromic craniosynostosis. Multiple alternatively spliced transcript variants encoding different isoforms have been noted for this gene. [provided by RefSeq, Jan 2009] Transcript Variant: This variant (9) is missing an in-frame coding exon, uses an alternate internal in-frame coding exon (as in variant 2) and an alternate 3' terminal exon, compared to transcript variant 1. This results in a shorter isoform (9), which differs in two internal segments, and has a novel C-terminus compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data because no quality transcript was available for the full length of the gene. The extent of this transcript is supported by transcript alignments. A downstream AUG translation start codon is selected for this RefSeq based on the presence of a strong Kozak consensus signal, a strong community standard for the use of the downstream start codon, and on a higher probability of an N-terminal signal peptide being present in the resulting protein. The use of an alternative in-frame upstream AUG start codon would result in a protein that is 19 aa longer at the N-terminus. Translation from the annotated downstream start codon is likely to occur via leaky scanning and/or reinitiation.