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Product datasheet for SC318304

FGFR2 (NM_022970) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	FGFR2 (NM_022970) 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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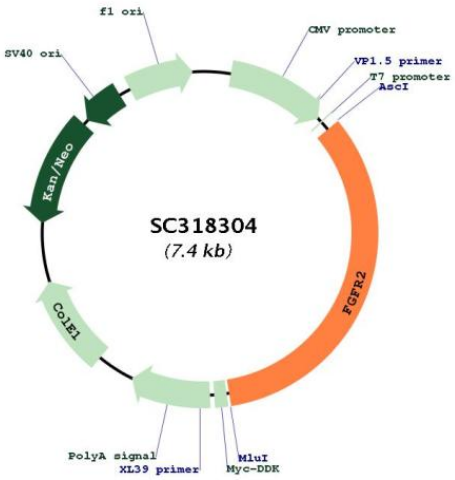
Fully Sequenced ORF:

>SC318304 representing NM_022970.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

GTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTA
CCGAGGAGATCTGCCGCCGCGATCGCCGGCGCGCCC
ATGGTCAGCTGGGGTCGTTTCATCTGCCTGGTCGTGGTCACCATGGCAACCTTGTCCCTGGCCCGGCCC
TCCTTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAAGAGCCACCAACCAAATACCAAATCTCTCAA
CCAGAAGTGTACGTGGCTGCGCCAGGGGAGTCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCGTG
ATCAGTTGGACTAAGGATGGGGTGCACTTGGGGCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTG
CAGATAAAGGGCGCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGACAGT
GAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGGATGACACCGAT
GGTGCGGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGAGCACCATACTGGACCAACACAGAAAAG
ATGGAAAAGCGGCTCCATGCTGTGCCTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGGAAC
CCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTAC
AAGGTACGAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTATACC
TGTGTAGTGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGATCGCCT
CACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGACGTAGAGTTT
GTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAGAACGGCAGT
AAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTCAAGCACTCGGGGATAAATAGTTCCAATGCA
GAAGTGCTGGCTCTGTTCAATGTGACCGAGGCGGATGCTGGGGAATATATATGTAAGGTCTCCAATTAT
ATAGGGCAGGCCAACCAGTCTGCCTGGCTCACTGTCCTGCCAAAACAGCAAGCGCCTGGAAGAGAAAAG
GAGATTACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCCTGT
ATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTCAGCAGCCAGCCG
GCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCC
TCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACACGCCTCTCTTCAACGGCAGACACCCCCATG
CTGGCAGGGGTCTCCGAGTATGAACTTCCAGAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACA
CTGGGCAAGCCCCTGGGAGAAGGTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAA
GACAAGCCCAAGGAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCTT
TCTGATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAAACACAAGAATATCATAAATCTTCTT
GGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGAGAA
TACCTCCGAGCCCGGAGGCCACCCGGGATGGAGTACTCCTATGACATTAACCGTGTTCCTGAGGAGCAG
ATGACCTTCAAGGACTTGGTGTCATGCACCTACCAGCTGGCCAGAGGCATGGAGTACTTGGCTTCCCAA
AAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCA
GACTTTGGACTCGCCAGAGATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCA
GTCAAGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTC
GGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCGTGGAGGAACTT
TTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCCAACTGCACCAACGAACTGTACATGATG
ATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACGTTCAAGCAGTTGGTAGAAGACTTGGAT
CGAATTCTCACTCTCACAACCAATGAGGAATACTTGGACCTCAGCCAACCTCTCGAACAGTATTCACCT
AGTTACCCTGACACAAGAAGTTCTTGTTCTTCAGGAGATGATTCTGTTTTTTCTCCAGACCCCATGCCT
TACGAACCATGCCTTCCTCAGTATCCACACATAAACGGCAGTGTTAAAACATGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites: AscI-MluI

Plasmid Map:



ACCN:	NM_022970
Insert Size:	2469 bp
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 custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery. The molecular sequence of this clone aligns with the gene accession number as a point of 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. More info
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_022970.3
RefSeq Size:	4657 bp
RefSeq ORF:	2469 bp
Locus ID:	2263
UniProt ID:	P21802
Cytogenetics:	10q26.13
Domains:	pkinase, TyrKc, S_TKc, ig, IGc2, IG
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:	92.1 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 (2) uses an alternate internal in-frame coding exon compared to transcript variant 1, resulting in an isoform (2, also known as isoform K-sam-IIH1, IIIb, and BFR-1) with a different, 1 aa longer protein segment in the mid-region compared to isoform 1.
Sequence Note: 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.
CCDS Note: A downstream AUG translation start codon is selected for this CCDS representation based on a strong community standard for its use, and on a higher probability of a signal peptide being present in the protein N-terminus. The use of an alternative upstream AUG start codon would result in a protein that is 19 aa longer at the N-terminus. The upstream AUG has a weak Kozak signal while the downstream AUG has a strong Kozak signal. Due to leaky scanning by ribosomes, it is possible that some ribosomes may initiate translation from the downstream AUG codon while others start from the upstream AUG. The presence of multiple upstream ORFs suggests that a combination of leaky scanning and translational reinitiation may be necessary to achieve translation of the annotated ORF.