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Product datasheet for SC302190

FANCA (NM_001018112) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	FANCA (NM_001018112) Human Untagged Clone
Tag:	Tag Free
Symbol:	FANCA
Synonyms:	FA; FA-H; FA1; FAA; FACA; FAH; FANCH
Mammalian Cell Selection:	None
Vector:	pCMV6-XL6
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF sequence for NM_001018112 edited ATGTCCGACTCGTGGGTCCCGAACTCCGCCTCGGGCCAGGACCCAGGGGGCCGCCGGAGG GCCTGGGCCGAGCTGCTGGCGGGAAGGGTCAAGAGGGAAAAATATAATCCTGAAAGGGCA CAGAAATTAAAGGAATCAGCTGTGCGCCTCCTGCGAAGCCATCAGGACCTGAATGCCCTT TTGCTTGAGGTAGAAGGTCCACTGTGTAAAAAATTGTCTCTCAGCAAAGTGATTGACTGT GACAGTTCTGAGGCCTATGCTAATCATTCTAGTTCATTTATAGGCTCTGCTTTGCAGGAT CAAGCCTCAAGGCTGGGGGTTCCCGTGGGTATTCTCTCAGCCGGGATGGTTGCCTCTAGC GTGGGACAGATCTGCACGGCTCCAGCGGAGACCAGTCACCCTGTGCTGCTGACTGTGGAG CAGAGAAAGAAGCTGTCTTCCCTGTTAGAGTTTGCTCAGTATTTATTGGCACACAGTATG TTCTCCCGTCTTTCCTTCTGTCAAGAATTATGGAAAATACAGAGTTCTTTGTTGCTTGAA GCGGTGTGGCATCTTCACGTACAAGGCATTGTGAGCCTGCAAGAGCTGCTGGAAAGCCAT CCCGACATGCATGCTGTGGGATCGTGGCTCTTCAGGAATCTGTGCTGCCTTTGTGAACAG ATGGAAGCATCCTGCCAGCATGCTGACGTCGCCAGGGCCATGCTTTCTGATTTTGTTCAA ATGTTTGTTTTGAGGGGATTTCAGAAAAACTCAGATCTGAGAAGAACTGTGGAGCCTGAA AAAATGCCGCAGGTCGCGGTTGATGTACTGCAGAGAATGCTGATTTTTGCACTTGACGCT TTGGCTGCTGGAGTACAGGAGGAGTCCTCCACTCACAAGATCGTGAGGTGCTGA
Restriction Sites:	Please inquire
ACCN:	NM_001018112
Insert Size:	1800 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:	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_001018112.1, NP_001018122.1
RefSeq Size:	1673 bp
RefSeq ORF:	894 bp
Locus ID:	2175
UniProt ID:	O15360
Cytogenetics:	16q24.3
Protein Families:	Druggable Genome
Gene Summary:	The Fanconi anemia complementation group (FANC) currently includes FANCA, FANCB, FANCC, FANCD1 (also called BRCA2), FANCD2, FANCE, FANCF, FANCG, FANCI, FANCJ (also called BRIP1), FANCL, FANCM and FANCN (also called PALB2). The previously defined group FANCH is the same as FANCA. Fanconi anemia is a genetically heterogeneous recessive disorder characterized by cytogenetic instability, hypersensitivity to DNA crosslinking agents, increased chromosomal breakage, and defective DNA repair. The members of the Fanconi anemia complementation group do not share sequence similarity; they are related by their assembly into a common nuclear protein complex. This gene encodes the protein for complementation group A. Alternative splicing results in multiple transcript variants encoding different isoforms. Mutations in this gene are the most common cause of Fanconi anemia. [provided by RefSeq, Jul 2008] Transcript Variant: This variant (2) contains an alternate exon, which results in an early stop codon, compared to variant 1. The resulting protein (isoform b) has a shorter C-terminus, compared to isoform a. 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.