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Product datasheet for SC112555

Fibrinogen alpha chain (FGA) (NM_021871) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Fibrinogen alpha chain (FGA) (NM_021871) Human Untagged Clone
Tag:	Tag Free
Symbol:	Fibrinogen alpha chain
Synonyms:	Fib2
Mammalian Cell Selection:	None
Vector:	pCMV6-XL4
E. coli Selection:	Ampicillin (100 ug/mL)

Fully Sequenced ORF:

>OriGene ORF within SC112555 sequence for NM_021871 edited (data generated by NextGen Sequencing)

ATGTTTTCCATGAGGATCGTCTGCCTGGTCCTAAGTGTGGTGGGCACAGCATGGACTGCA
GATAGTGGTGAAGGTGACTTTCTAGCTGAAGGAGGAGGCGTGCGTGGCCCAAGGGTTGTG
GAAAGACATCAATCTGCCTGCAAAGATTCAGACTGGCCCTTCTGCTCTGATGAAGACTGG
AACTACAAATGCCCTTCTGGCTGCAGGATGAAAGGGTTGATTGATGAAGTCAATCAAGAT
TTTACAAACAGAATAAATAAGCTCAAAAATTCACTATTTGAATATCAGAAGAACAATAAG
GATTCTCATTCGTTGACCACTAATATAATGGAAATTTTGAGAGGCGATTTTTCCTCAGCC
AATAACCGTGATAATACCTACAACCGAGTGTCAGAGGATCTGAGAAGCAGAATTGAAGTC
CTGAAGCGCAAAGTCATAGAAAAAGTACAGCATATCCAGCTTCTGCAGAAAAATGTTAGA
GCTCAGTTGGTTGATATGAAACGACTGGAGGTGGACATTGATATTAAGATCCGATCTTGT
CGAGGGTCATGCAGTAGGGCTTTAGCTCGTGAAGTAGATCTGAAGGACTATGAAGATCAG
CAGAAGCAACTTGAACAGGTCATTGCCAAAGACTTACTTCCCTCTAGAGATAGGCAACAC
TTACCACTGATAAAAATGAAACCAGTTCCAGACTTGGTTCCCGGAAATTTTAAGAGCCAG
CTTCAGAAGGTACCCCCAGAGTGGAAGGCATTAACAGACATGCCGCAGATGAGAATGGAG
TTAGAGAGACCTGGTGGAAATGAGATTACTCGAGGAGGCTCCACCTCTTATGGAACCGGA
TCAGAGACGGAAAGCCCCAGGAACCCTAGCAGTGCTGGAAGCTGGAACTCTGGGAGCTCT
GGACCTGGAAGTACTGGAAACCGAAACCCTGGGAGCTCTGGGACTGGAGGGACTGCAACC
TGGAAACCTGGGAGCTCTGGACCTGGAAGTGCTGGAAGCTGGAACTCTGGGAGCTCTGGA
ACTGGAAGTACTGGAAACCAAAACCCTGGGAGCCCTAGACCTGGTAGTACCGGAACCTGG
AATCCTGGCAGCTCTGAACGCGGAAGTGCTGGGCACTGGACCTCTGAGAGCTCTGTATCT
GGTAGTACTGGACAATGGCACTCTGAATCTGGAAGTTTTAGGCCAGATAGCCCAGGCTCT
GGGAACGCGAGGCCTAACAACCCAGACTGGGGCACATTTGAAGAGGTGTCAGGAAATGTA
AGTCCAGGGACAAGGAGAGAGTACCACACAGAAAAACTGGTCACTTCTAAAGGAGATAAA
GAGCTCAGGACTGGTAAAGAGAAGGTCACCTCTGGTAGCACAACCACCACGCGTCGTTCA
TGCTCTAAAACCGTTACTAAGACTGTTATTGGTCCTGATGGTCACAAAGAAGTTACCAAA
GAAGTGGTGACCTCCGAAGATGGTTCTGACTGTCCCGAGGCAATGGATTTAGGCACATTG
TCTGGCATAGGTACTCTGGATGGGTTCCGCCATAGGCACCCTGATGAAGCTGCCTTCTTC
GACACTGCCTCAACTGGAAAAACATTCCCAGGTTTCTTCTCACCTATGTTAGGAGAGTTT
GTCAGTGAGACTGAGTCTAGGGGCTCAGAATCTGGCATCTTCACAAATACAAAGGAATCC
AGTTCTCATCACCCTGGGATAGCTGAATTCCCTTCCCGTGGTAAATCTTCAAGTTACAGC
AAACAATTTACTAGTAGCACGAGTTACAACAGAGGAGACTCCACATTTGAAAGCAAGAGC
TATAAAATGGCAGATGAGGCCGGAAGTGAAGCCGATCATGAAGGAACACATAGCACCAAG
AGAGGCCATGCTAAATCTCGCCCTGTCAGAGGTATCCACACTTCTCCTTTGGGGAAGCCT
TCCCTGTCCCCCTAG

Clone variation with respect to NM_021871.2
991 a=>g

5' Read Nucleotide Sequence:

>OriGene 5' read for NM_021871 unedited
GCACGAGGAGTGCTCCTCAGNAGCCAGCCCCACCCTTAGAAAAATGTTTTCCATTGAGGA
TCGTCTGCCTGGTCCTAAGTGTGGTGGGCACAGCATGGACTGCAGATAGTGGTGA

3' Read Nucleotide Sequence:

>OriGene 3' read for NM_021871 unedited
NAATCTTTGNNACCGCGGCCGCAATCTAGNATCGAGNTTTTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTCCATTAAACATGAATTTATTGAGTCATGGCTCTGTACTGTTAGGCATTTGG
GAATACAGAGATGAAACAGACAAAGGCCCTGCCCCCAAGGAACTTACAGTCTAGCACAAA
AACAGACCAAAAAAGGGTAGTTTCAATGACGTGTAACAGAGAGTTAAAAAGGAAATGCAG
GGGGCCATGGGAACACTGGGCAAAAATATTTAACTTAGTCTAGGGGGACAGGGAAGGCTT
CCCCAAAGGAAAAGGGGGGATACCTCTGACAGGGCGAGATTTACCATGGCCTCTCTTGGG
GCTATGGGTTCCTTCATGATCGGCTTCACTTCCGGCCTCATCTGCCATTTTATAGCTCTT
GCTTTCAAATGTGGAGTCTCCTCTGTTGAAACTCGGGCTACTAGTAAATTGTTTGCTGTA
ACTTGAAGATTTACCACGGGAAGGGAATTCAGCTATCCCAGGGTGATGAGAACTGGATTC
CTTTGTATTTGTGAAAATGCCAAATTCTGAGCCCCTAGACTCAGTCTCACTGACAAACTC
TCCTAACATAGGTGAGAAGAAACCTGGGAATGTTTTTCCAGTTGAGGCAGTGTCAAAGAA
GGCAGCTTCATCAGGGTGCCTATGGCGGAACCCATCCAGAGTACCTATGCCAGACAATGT
GCCTAAATCCATTGCCTCGGGACAGTCAGAACCATCTTCGGAGGTCACCACTTCTTTGGT
AACTTCTTTGNGACCATCAGGACCATTACAGTCTTAGTAACGGNTTTAGAGCATGAACGA
CGCGTGGTGGGTTGGGCTACCAGAGGGTGACTTNCTCTTAACNAGTCCTGAGCTCTTTAT
CTCTTTAGAAGTGACCAGTTTTNCTGTGNGGNACTCTCTCCTTGNCCCTGGAACTAACAT
TNCTGACACTT

Restriction Sites: NotI-NotI

ACCN: NM_021871

Insert Size: 2210 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).

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_021871.2, NP_068657.1

RefSeq Size: 2210 bp

RefSeq ORF: 1935 bp

Locus ID: 2243

UniProt ID: P02671

Cytogenetics: 4q31.3

Protein Families: Druggable Genome, Secreted Protein

Protein Pathways: Complement and coagulation cascades

Gene Summary: This gene encodes the alpha subunit of the coagulation factor fibrinogen, which is a component of the blood clot. Following vascular injury, the encoded preproprotein is proteolytically processed by thrombin during the conversion of fibrinogen to fibrin. Mutations in this gene lead to several disorders, including dysfibrinogenemia, hypofibrinogenemia, afibrinogenemia and renal amyloidosis. Alternative splicing results in multiple transcript variants, at least one of which encodes an isoform that undergoes proteolytic processing. [provided by RefSeq, Jan 2016]
Transcript Variant: This variant (alpha) is alternatively spliced in the 3' coding region and 3' UTR, resulting in a shorter isoform (alpha) with a different carboxy-terminus compared to isoform alpha-E. The encoded isoform (alpha) may undergo proteolytic processing similar to isoform alpha-E. 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.