

## Product datasheet for **SC119634**

### GGCX (NM\_000821) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	GGCX (NM_000821) Human Untagged Clone
Tag:	Tag Free
Symbol:	GGCX
Synonyms:	VKCFD1
Mammalian Cell Selection:	None
Vector:	<u><a href="#">pCMV6-XL5</a></u>
E. coli Selection:	Ampicillin (100 ug/mL)



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Fully Sequenced ORF: >OriGene ORF within SC119634 sequence for NM\_000821 edited (data generated by NextGen Sequencing)

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ATGGCGGTGTCTGCCGGTCCGCGCGGACCTCGCCCAGCTCAGATAAAGTACAGAAAGAC
AAGGCTGAACTGATCTCAGGGCCAGGCAGGACAGCCGAATAGGGAAACTCTTGGGTTTT
GAGTGGACAGATTTGTCCAGTTGGCGGAGGCTGGTGACCCTGTGAATCGACCAACGGAC
CCTGCAAGCTTAGCTGTCTTTCTTTTGGTTCTTGATGGTGCTAGACATTCCC
CAGGACGCGGGGCTCAGCTCTCTGGACCAGAAATACCTGATGGGCTGGATGTGTGCCG
TTCCCTTGCTGGATGCCCTACGCCCACTGCCACTTGACTGGATGTATCTTGTCTACACC
ATCATGTTTCTGGGGCACTGGGCATGATGCTGGGCTGTGCTACCGGATAAGCTGTGTG
TTATTCCTGCTGCCATACTGGTATGTGTTCTCCTGGACAAGACATCATGGAACAACCAC
TCCTATCTGTATGGGTTGTTGGCCTTTCAGCTAACATTTCATGGATGCAAACCACTACTGG
TCTGTGGACGGTCTGCTGAATGCCCATAGGAGGAATGCCACGTGCCCTTTGAACTAT
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GCAGACTGGGTTGAAGGCTATTCATGGAATATTTGCCCGCACTGGCTCTTCAGTCCC
TTCAAAGTGTGTGCTGAGGAGCTGACTAGCCTGCTGGTCTGCACTGGGGTGGGCTG
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TTCTTTGTGCCTACTTCCACTGCATGAATCCAGCTTTTCAGCATTGGTATGTCTCC
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TTCTTCCGCTTCTTGTGCGAAAGCTCTATGTCTTTGCCCGCAGCTTCTGATGACTTGT
ATCTCACTTCGAAATCTGATATTAGCCGCTCTCCCTGGAGCAGCTGGCCCAGGAGGTG
ACTTATGCAAACCTTGAGACCCTTTGAGGCAGTTGGAGAAGTGAATCCCTCAAACACGGAT
TCTTCACATTCTAATCCTCCTGAGTCAAATCCTGATCCTGTCCACTCAGAGTTCTGA
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Clone variation with respect to NM\_000821.5  
974 g=>a;1218 c=>t

<b>5' Read Nucleotide Sequence:</b>	<p>&gt;OriGene 5' read for NM_000821 unedited</p> <pre> NGTTTCAGCATTTTGTAAATACGACTCACTTATAGGGCGGCCGCGATTTCGGCACGAGGCC ACCTGCCTCCTCCGCAGAGCAATGGCGGTGTCTGCCGGTCCGCGCGGACCTCGCCCAGC TCAGATAAAGTACAGAAAGACAAGGCTGAACTGATCTCAGGGCCAGGCAGGACAGCCGA ATAGGGAAACTCTTGGGTTTTGAGTGGACAGATTGTCCAGTTGGCGGAGGCTGGTGACC CTGCTGAATCGACCAACGACCCTGCAAGCTTAGCTGTCTTTCTTTTGGGTTT TTGATGGTGTAGACATTCGCCAGGAGCGGGGCTCAGCTCTCTGGACCGAAAACCTT GATGGGCTGGATGTGTGCCGCTTCCCCTTGTCTGGATGCCCTACGCCCACTGCCACTTGAC TGGATGTATCTTGTCTACACCATCATGTTTCTGGGGCACTGGGCATGATGCTGGGCCTG TGCTACCGGATAAGCTGTGTGTTATTCCTGCTGCCATACTGGTATGTGTTTCTCCTGGAC AAGACATCATGGAACAACCACTCCTATCTGTATGGGTTGTTGGCCTTTCAGCTAACATTC ATGGATGCAAACCACTACTGGTCTGTGGACGGTCTGCTGAATGCCCATAGGAGGAATGCC CACGTGCCCTTTGGAATATGCAGTGTCCGTGGCCAGATCTTCATTGTGACTTCATT GCGGGTGTAAAAAGCTGGATGCAGACTGGGTTGAAGCTATTCCATGGAATAATTGTCCC GCACTGGCTCTTCAGTCCCTTCAACTGCTGTTGTCTGAAGAGCTGACTANCCTGTGTTT GTGCACTGGGGTGGGCTGCTGCTTGACCTCTCAGCTGGTTTCTGCTCTTNTTGTATGCTC AAGACCATTGGCCTGTCTTTGGGCTACTTCCA </pre>
<b>3' Read Nucleotide Sequence:</b>	<p>&gt;OriGene 3' read for NM_000821 unedited</p> <pre> CTATGGACCGCGCCGCAATCTAGGATCGAGTTTTTTTTTTTTTTTTTTTGGCACTTTAT TTATTTATTTATTTTGGACGAAGTCTTGCTCTGTTGCCAGGAGTGCAGTGGCTCGATC TCGGCTCACTGCAACCTCCACCTCCTGGGCCCAAGCGATTCTCATGCCTCAGCCTCCTGG GTAGTTGGATTACAGGCACCCACCACAGTCTGGCTAATTTTTGTATTTTGTAGTGTAGAGA AGGGGTCTTGCCATGTTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAAGTGATCTGCCCA CCTCAGCCTCCCAAAATGCTGGGATTACAGGCGTGAGCCACGGCACCCAGCCCCCAAAAA GCCACTTTAAACCTTATCCTAGGAGGACAGTTTACATTGCGTCTAACCTCTTCTCGGCC TCTTAATCTTGGGTTGTTAAATCTTATTTGCTTATTTCTTGGTTCTCTAAGTTGTAA TCTCGGAGTTAAAAACAGCTTTAGAACCCCGCCCCCAAAAAAAAAAAAAAAAAAACTTTT GAGAATTTTTTTCAAATAAATGTCCATTGCATAGAATGGGTCTGTGACTGGCTGCTTCTA CATCTGCACCCCAACATCTGGCCCCCTTCAAGACTCTGAGTGGACAGGATCAGGATTTGAC TCANGAGGATTAGAATGTGAAGAATCCGTGTTTGAAGGATTAGTTCTCCAACCTGCCTCA AAGGGTCTCAAGTTTGCATAAGTCACCTCCTGGGCCAGCTGCCTCCAGGAAGGACGGCCT AATATCAGATTTGAAAGTGAGATACAAGTCATCAGGAACCTGCGGCGAAAGAATAGAGCT TTCGCAACAGAAGCGGAGAATCGCTCATGGAAAGGAGTATTTTCGCCGCTTTCATCTCCT GGAGCCTTTGTTGCGTCTAAGAAAGTCTGACCAGAGGGTTGCCTCAGNCCCCCTAACTT CCCTCCACAGAGCTGCGT </pre>
<b>Restriction Sites:</b>	NotI-NotI
<b>ACCN:</b>	NM_000821
<b>Insert Size:</b>	2940 bp
<b>OTI Disclaimer:</b>	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).
<b>Components:</b>	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\\_000821.3](#), [NP\\_000812.2](#)

**RefSeq Size:** 3236 bp

**RefSeq ORF:** 2277 bp

**Locus ID:** 2677

**UniProt ID:** [P38435](#)

**Cytogenetics:** 2p11.2

**Domains:** VKG\_Carbox

**Protein Families:** Druggable Genome, Transmembrane

**Gene Summary:** This gene encodes an integral membrane protein of the rough endoplasmic reticulum that carboxylates glutamate residues of vitamin K-dependent proteins to gamma carboxyl glutamate, a modification that is required for their activity. The vitamin K-dependent protein substrates have a propeptide that binds the enzyme, with carbon dioxide, dioxide, and reduced vitamin K acting as co-substrates. Vitamin K-dependent proteins affect a number of physiologic processes including blood coagulation, prevention of vascular calcification, and inflammation. Allelic variants of this gene have been associated with pseudoxanthoma elasticum-like disorder with associated multiple coagulation factor deficiency. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Aug 2015]  
Transcript Variant: This variant (1) represents the longest transcript and encodes the longest isoform (1). 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.