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Cancer gene Research Literatures

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Abstract: Cancer is the general name for a group of more than 100 diseases. Although there are many kinds of cancer, all cancers start because abnormal cells grow out of control. Untreated cancers can cause serious illness and death. The body is made up of trillions of living cells. Normal body cells grow, divide, and die in an orderly fashion. During the early years of a person's life, normal cells divide faster to allow the person to grow. After the person becomes an adult, most cells divide only to replace worn-out or dying cells or to repair injuries. This article introduces recent research reports as references in the related studies.

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Key words: cancer; life; research; literature; cell; gene

1. Introduction

Cancer is the general name for a group of more than 100 diseases. Although there are many kinds of cancer, all cancers start because abnormal cells grow out of control. Untreated cancers can cause serious illness and death. The body is made up of trillions of living cells. Normal body cells grow, divide, and die in an orderly fashion. During the early years of a person's life, normal cells divide faster to allow the person to grow. After the person becomes an adult, most cells divide only to replace worn-out or dying cells or to repair injuries.

The following introduces genes related to cancers as references in the related studies.

Homo sapiens phosphatase and tensin homolog (PTEN), transcript variant 1, mRNA

NCBI Reference Sequence: NM_000314.6

LOCUS NM_000314 8718 bp mRNA linear PRI 18-NOV-2018

DEFINITION Homo sapiens phosphatase and tensin homolog (PTEN), transcript variant 1, mRNA.

ACCESSION NM_000314

VERSION NM_000314.6

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 8718)

AUTHORS Li AG, Murphy EC, Culhane AC, Powell E, Wang H, Bronson RT, Von T, Giobbie-Hurder A, Gelman RS, Briggs KJ, Piwnica-Worms H, Zhao JJ, Kung AL, Kaelin WG Jr and Livingston DM.

TITLE BRCA1-IRIS promotes human tumor progression through PTEN blockade and HIF-1alpha activation

JOURNAL Proc Natl Acad Sci U S A 115 (41), E9600-E9609 (2018)

PUBMED [30254159](#)

REMARK GeneRIF: The IRIS-driven metastatic mechanism results from IRIS-dependent suppression of phosphatase and tensin homolog (PTEN) transcription, which in turn perturbs the PI3K/AKT/GSK-3beta pathway leading to prolyl hydroxylase-independent HIF-1alpha

stabilization and activation in a normoxic environment.

REFERENCE 2 (bases 1 to 8718)

AUTHORS Jouali F, Marchoudi N, Talbi S, Bilal B, El Khasmi M, Rhaissi H and Fekkak J.

TITLE Detection of PIK3/AKT pathway in Moroccan population with triple negative breast cancer

JOURNAL BMC Cancer 18 (1), 900 (2018)

PUBMED [30227836](#)

REMARK GeneRIF: In this study, we used the Ion Personal Genome Machine (PGM) and Ion Torrent Ampliseq Cancer panel to sequence hotspot regions from PIK3CA, AKT and PTEN genes to identify genetic mutations in 39 samples of TNBC subtype from Moroccan patients and to correlate the results with clinical-pathologic data

Publication Status: Online-Only

REFERENCE 3 (bases 1 to 8718)

AUTHORS Li W, Zhang T, Guo L and Huang L.

TITLE Regulation of PTEN expression by noncoding RNAs

JOURNAL J Exp Clin Cancer Res 37 (1), 223 (2018)

PUBMED [30217221](#)

REMARK GeneRIF: we provide a review on current understandings of the regulation of PTEN by ncRNAs, which could contribute to the development of novel approaches to the diseases with abnormal expression of PTEN.

Review article

Publication Status: Online-Only

REFERENCE 4 (bases 1 to 8718)

AUTHORS Xu W, Yang Z, Xie C, Zhu Y, Shu X, Zhang Z, Li N, Chai N, Zhang S, Wu K, Nie Y and Lu N.

TITLE PTEN lipid phosphatase inactivation links the hippo and PI3K/Akt pathways to induce gastric tumorigenesis

JOURNAL J Exp Clin Cancer Res 37 (1), 198 (2018)

PUBMED [30134988](#)

REMARK GeneRIF: PTEN lipid phosphatase inactivation abolished the MOB1-LATS1/2 interaction, decreased YAP phosphorylation and finally promoted YAP nuclear translocation, which enhanced the synergistic effect of YAP-TEAD, thus inducing cell proliferation and migration.

Publication Status: Online-Only

REFERENCE 5 (bases 1 to 8718)

AUTHORS Liang H, He S, Yang J, Jia X, Wang P, Chen X, Zhang Z, Zou X, McNutt MA, Shen WH and Yin Y.

TITLE PTENalpha, a PTEN isoform translated through alternative initiation, regulates mitochondrial function and energy metabolism

JOURNAL Cell Metab 19 (5), 836-848 (2014)

PUBMED [24768297](#)

REFERENCE 6 (bases 1 to 8718)

AUTHORS Hopkins BD, Fine B, Steinbach N, Dendy M, Rapp Z, Shaw J, Pappas K,

Yu JS, Hodakoski C, Mense S, Klein J, Pegno S, Sulis ML, Goldstein

H, Amendolara B, Lei L, Maurer M, Bruce J, Canoll P, Hibshoosh H

and Parsons R.

TITLE A secreted PTEN phosphatase that enters cells to alter signaling and survival

JOURNAL Science 341 (6144), 399-402 (2013)

PUBMED [23744781](#)

REMARK GeneRIF: identified a 576-amino acid translational variant of PTEN,

PTEN-Long, that arises from an alternative translation start site

519 base pairs upstream of the ATG initiation sequence; PTEN-Long

is a membrane-permeable lipid phosphatase that is secreted from cells and can enter other cells

REFERENCE 7 (bases 1 to 8718)

AUTHORS Steck PA, Pershouse MA, Jasser SA, Yung WK, Lin H, Ligon AH, Langford LA, Baumgard ML, Hattier T, Davis T, Frye C, Hu R, Swedlund B, Teng DH and Tavtigian SV.

TITLE Identification of a candidate tumour suppressor gene, MMAC1, at chromosome 10q23.3 that is mutated in multiple advanced cancers

JOURNAL Nat Genet 15 (4), 356-362 (1997)

PUBMED [9090379](#)

REFERENCE 8 (bases 1 to 8718)

AUTHORS Li J, Yen C, Liaw D, Podsypanina K, Bose S, Wang SI, Puc J, Miliareis C, Rodgers L, McCombie R, Bigner SH, Giovanella BC, Ittmann M, Tycko B, Hibshoosh H, Wigler MH and Parsons R.

TITLE PTEN, a putative protein tyrosine phosphatase gene mutated in human brain, breast, and prostate cancer

JOURNAL Science 275 (5308), 1943-1947 (1997)

PUBMED [9072974](#)

REFERENCE 9 (bases 1 to 8718)

AUTHORS Peiffer SL, Herzog TJ, Tribune DJ, Mutch DG, Gersell DJ and Goodfellow PJ.

TITLE Allelic loss of sequences from the long arm of chromosome 10 and replication errors in endometrial cancers

JOURNAL Cancer Res 55 (9), 1922-1926 (1995)

PUBMED [7728760](#)

REFERENCE 10 (bases 1 to 8718)

AUTHORS Eng,C.

TITLE PTEN Hamartoma Tumor Syndrome

JOURNAL (in) Adam MP, Ardiserger HH, Pagon RA, Wallace SE, Bean LJH, Stephens K and Amemiya A (Eds.); GENEREVIEWS(R); (1993)

PUBMED [20301661](#)

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [U92436.1](#), [AC063965.8](#), [BC005821.2](#) and [AA836562.1](#).

[WARNING] On Nov 21, 2018 this sequence was replaced by [NM_000314.7](#).

On Mar 25, 2015 this sequence version replaced [NM_000314.5](#).

Summary: This gene was identified as a tumor suppressor that is mutated in a large number of cancers at high frequency. The protein encoded by this gene is a phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase. It contains a tensin like domain as well as a catalytic domain similar to that of the dual specificity protein tyrosine phosphatases. Unlike most of the protein tyrosine phosphatases, this protein preferentially dephosphorylates phosphoinositide substrates. It negatively regulates intracellular levels of phosphatidylinositol-3,4,5-trisphosphate in cells and functions as a tumor suppressor by negatively regulating AKT/PKB signalling pathway. The use of a non-canonical (CUG) upstream initiation site produces a longer isoform that initiates translation with a leucine, and is thought to be preferentially associated with the mitochondrial inner membrane. This longer isoform may help regulate energy metabolism in the mitochondria. A pseudogene of this gene is found on chromosome 9. Alternative

splicing and the use of multiple translation start codons results in multiple transcript variants encoding different isoforms.
[provided by RefSeq, Feb 2015].

Transcript Variant: This variant (1) encodes multiple isoforms due to the use of alternative translation initiation codons. The longest isoform (PTEN-L, PMID:23744781; also known as PTENalpha, PMID: 24768297) is derived from the use of an upstream non-AUG (CUG) start codon, while two shorter isoforms are derived from downstream AUG start codons. The most abundant isoform (PTEN), which is derived from the use of the 5'-most AUG start codon, is represented in this RefSeq.

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.

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: U92436.1, SRR1660807.191185.1
[ECO:000032]

RNAseq introns :: single sample supports all introns
SAMEA1965299, SAMEA1966682
[ECO:0000348]

##Evidence-Data-END##

##RefSeq-Attributes-START##

CDS uses downstream in-frame AUG :: experimental evidence
(PMID:24768297)

##RefSeq-Attributes-END##

COMPLETENESS: complete on the 3' end.

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130-195	U92436.1	130-195		
196-2253	BC005821.2	1-2058		
2254-8472	AC063965.8	77056-83274	c	
8473-8718	AA836562.1	2-247	c	

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Homo sapiens mortality factor 4 like 1 (MORF4L1), transcript variant 4, mRNA

NCBI Reference Sequence: NM_001265604.2

[FASTA Graphics](#)

[Go to:](#)

LOCUS NM_001265604 2333 bp mRNA linear PRI 16-DEC-2020

DEFINITION Homo sapiens mortality factor 4 like 1 (MORF4L1), transcript variant 4, mRNA.

ACCESSION NM_001265604

VERSION NM_001265604.2

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2333)

AUTHORS Fragoza R, Das J, Wierbowski SD, Liang J, Tran TN, Liang S, Beltran JF, Rivera-Erick CA, Ye K, Wang TY, Yao L, Mort M, Stenson PD, Cooper DN, Wei X, Keinan A, Schimenti JC, Clark AG and Yu H.

TITLE Extensive disruption of protein interactions by genetic variants across the allele frequency spectrum in human populations

JOURNAL Nat Commun 10 (1), 4141 (2019)

PUBMED [31515488](#)

REMARK Publication Status: Online-Only

REFERENCE 2 (bases 1 to 2333)

AUTHORS Hou P, Huang C, Liu CP, Yang N, Yu T, Yin Y, Zhu B and Xu RM.

TITLE Structural Insights into Stimulation of Ash1L's H3K36

Methyltransferase Activity through Mrg15 Binding

JOURNAL Structure 27 (5), 837-845 (2019)

PUBMED [30827843](#)

REMARK GeneRIF: Ash1L stimulates H3K36 methyltransferase activity through Mrg15 binding

REFERENCE 3 (bases 1 to 2333)

AUTHORS Lee Y, Yoon E, Cho S, Schmahling S, Muller J and Song JJ.

TITLE Structural Basis of MRG15-Mediated Activation of the ASH1L Histone

Methyltransferase by Releasing an Autoinhibitory Loop

JOURNAL Structure 27 (5), 846-852 (2019)

PUBMED [30827841](#)

REMARK GeneRIF: ASH1L activation by MRG15 represents a delicate regulatory mechanism for how a cofactor activates an SET domain HMTase by releasing autoinhibition

REFERENCE 4 (bases 1 to 2333)

AUTHORS Bleuyard JY, Fournier M, Nakato R, Couturier AM, Katou Y, Ralf C,

Hester SS, Dominguez D, Rhodes D, Humphrey TC, Shirahige K and

Esashi F.

TITLE MRG15-mediated tethering of PALB2 to unperturbed chromatin protects active genes from genotoxic stress

JOURNAL Proc Natl Acad Sci U S A 114 (29), 7671-7676 (2017)

PUBMED [28673974](#)

REMARK GeneRIF: PALB2 associates with active genes through its major binding partner, MRG15, which recognizes histone H3 trimethylated at lysine 36 (H3K36me3) by the SETD2 methyltransferase

REFERENCE 5 (bases 1 to 2333)

AUTHORS Marcon E, Ni Z, Pu S, Turinsky AL, Trimble SS, Olsen JB, Silverman-Gavrila R, Silverman-Gavrila L, Phanse S, Guo H, Zhong G, Guo X, Young P, Bailey S, Roudeva D, Zhao D, Hewel J, Li J, Graslund S, Paduch M, Kossiakoff AA, Lupien M, Emili A, Wodak SJ and Greenblatt J.

TITLE Human-chromatin-related protein interactions identify a demethylase complex required for chromosome segregation

JOURNAL Cell Rep 8 (1), 297-310 (2014)

PUBMED [24981860](#)

REFERENCE 6 (bases 1 to 2333)

AUTHORS Cai Y, Jin J, Tomomori-Sato C, Sato S, Sorokina I, Parmely TJ, Conaway RC and Conaway JW.

TITLE Identification of new subunits of the multiprotein mammalian TRRAP/TIP60-containing histone acetyltransferase complex

JOURNAL J Biol Chem 278 (44), 42733-42736 (2003)

PUBMED [12963728](#)

REFERENCE 7 (bases 1 to 2333)

AUTHORS Pardo PS, Leung JK, Lucchesi JC and Pereira-Smith OM.

TITLE MRG15, a novel chromodomain protein, is present in two distinct multiprotein complexes involved in transcriptional activation

JOURNAL J Biol Chem 277 (52), 50860-50866 (2002)

PUBMED [12397079](#)

REMARK GeneRIF: a novel chromodomain protein that is present in two distinct multiprotein complexes involved in transcriptional activation

REFERENCE 8 (bases 1 to 2333)

AUTHORS Yochum GS and Ayer DE.

TITLE Role for the mortality factors MORF4, MRGX, and MRG15 in transcriptional repression via associations with Pfl, mSin3A, and Transducin-Like Enhancer of Split

JOURNAL Mol Cell Biol 22 (22), 7868-7876 (2002)

PUBMED [12391155](#)

REFERENCE 9 (bases 1 to 2333)

AUTHORS Leung JK, Berube N, Venable S, Ahmed S, Timchenko N and Pereira-Smith OM.

TITLE MRG15 activates the B-myb promoter through formation of a nuclear complex with the retinoblastoma protein and the novel protein PAM14

JOURNAL J Biol Chem 276 (42), 39171-39178 (2001)

PUBMED [11500496](#)

REFERENCE 10 (bases 1 to 2333)

AUTHORS Bertram MJ, Berube NG, Hang-Swanson X, Ran Q, Leung JK, Bryce S, Spurgers K, Bick RJ, Baldini A, Ning Y, Clark LJ, Parkinson EK, Barrett JC, Smith JR and Pereira-Smith OM.

TITLE Identification of a gene that reverses the immortal phenotype of a subset of cells and is a member of a novel family of transcription factor-like genes

JOURNAL Mol Cell Biol 19 (2), 1479-1485 (1999)

PUBMED [9891081](#)

COMMENT VALIDATED [REFSEQ](#): This record has undergone validation or preliminary review. The reference sequence was derived from

[AC103975.9](#), [DB455429.1](#), [AK300789.1](#), [AY148481.1](#), [BM996530.1](#) and [AC011944.12](#).

On Aug 13, 2020 this sequence version replaced [NM_001265604.1](#).

Transcript Variant: This variant (4) differs in the 5' UTR and

initiates translation at a downstream, in-frame start codon, compared to variant 1. Variants 3, 4 and 5 encode the same isoform (3), which has a shorter N-terminus compared to isoform 1.

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: AK300789.1, SRR1660805.249535.1
[ECO:0000332]

##Evidence-Data-END##

COMPLETENESS: complete on the 3' end.

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Homo sapiens suppressor of cytokine signaling 3 (SOCS3), transcript variant 3, mRNA

NCBI Reference Sequence: NM_001378933.1

[FASTA Graphics](#)[Go to:](#)

LOCUS NM_001378933 2476 bp mRNA linear PRI 15-DEC-2020

DEFINITION Homo sapiens suppressor of cytokine signaling 3 (SOCS3), transcript variant 3, mRNA.

ACCESSION NM_001378933

VERSION NM_001378933.1

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

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 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2476)

AUTHORS Johnson HM, Lewin AS and Ahmed CM.

TITLE SOCS, Intrinsic Virulence Factors, and Treatment of COVID-19

JOURNAL Front Immunol 11, 582102 (2020)

[PUBMED 33193390](#)

REMARK GeneRIF: SOCS, Intrinsic Virulence Factors, and Treatment of COVID-19.

Review article

Publication Status: Online-Only

REFERENCE 2 (bases 1 to 2476)

AUTHORS Jiang M, Zhang W, Zhang R, Liu P, Ye Y, Yu W, Guo X and Yu J.

TITLE Cancer exosome-derived miR-9 and miR-181a promote the development of early-stage MDSCs via interfering with SOCS3 and PIAS3 respectively in breast cancer

JOURNAL Oncogene 39 (24), 4681-4694 (2020)

PUBMED [32398867](#)

REMARK GeneRIF: Cancer exosome-derived miR-9 and miR-181a promote the development of early-stage MDSCs via interfering with SOCS3 and PIAS3 respectively in breast cancer.

REFERENCE 3 (bases 1 to 2476)

AUTHORS Luck K, Kim DK, Lambourne L, Spirohn K, Begg BE, Bian W, Brignall R, Cafarelli T, Campos-Laborie FJ, Charlotteaux B, Choi D, Cote AG, Daley M, Deimling S, Desbuleux A, Dricot A, Gebbia M, Hardy MF, Kishore N, Knapp JJ, Kovacs IA, Lemmens I, Mee MW, Mellor JC, Pollis C, Pons C, Richardson AD, Schlabach S, Teeking B, Yadav A, Babor M, Balcha D, Basha O, Bowman-Colin C, Chin SF, Choi SG, Colabella C, Coppin G, D'Amata C, De Ridder D, De Rouck S, Duran-Frigola M, Ennajdaoui H, Goebels F, Goehring L, Gopal A, Haddad G, Hatchi E, Helmy M, Jacob Y, Kassa Y, Landini S, Li R, van Lieshout N, MacWilliams A, Markey D, Paulson JN, Rangarajan S, Rasla J, Rayhan A, Rolland T, San-Miguel A, Shen Y, Sheykharimli D, Sheynkman GM, Simonovsky E, Tasan M, Tejeda A, Tropepe V, Twizere JC, Wang Y, Weatheritt RJ, Weile J, Xia Y, Yang X, Yeger-Lotem E, Zhong Q, Aloy P, Bader GD, De Las Rivas J, Gaudet S, Hao T, Rak J, Tavernier J, Hill DE, Vidal M, Roth FP and Calderwood MA.

TITLE A reference map of the human binary protein interactome

JOURNAL Nature 580 (7803), 402-408 (2020)

PUBMED [32296183](#)

REFERENCE 4 (bases 1 to 2476)

AUTHORS Yang Z, Zhu H, Zhang L, Wei Q, Zhou L, Xu X, Song P, Liu J, Xie H and Zheng S.

TITLE DNA methylation of SOCS1/2/3 predicts hepatocellular carcinoma recurrence after liver transplantation

JOURNAL Mol Biol Rep 47 (3), 1773-1782 (2020)

PUBMED [32006198](#)

REMARK GeneRIF: DNA methylation of SOCS1/2/3 predicts hepatocellular carcinoma recurrence after liver transplantation.

REFERENCE 5 (bases 1 to 2476)

AUTHORS Sun Y, Ju XL, Li D, Zhou PP, Li X and Luo RH.

TITLE RETRACTED: miR-1290 promotes proliferation and suppresses apoptosis in acute myeloid leukemia by targeting FOXG1/SOCS3

JOURNAL J Biol Regul Homeost Agents 33 (6) (2019)

PUBMED [31960662](#)

REMARK GeneRIF: miR-1290 promoted proliferation and suppressed apoptosis in acute myeloid leukemia by targeting FOXG1 and SOCS3

REFERENCE 6 (bases 1 to 2476)

AUTHORS Marine JC, McKay C, Wang D, Topham DJ, Parganas E, Nakajima H, Pendeville H, Yasukawa H, Sasaki A, Yoshimura A and Ihle JN.

TITLE SOCS3 is essential in the regulation of fetal liver erythropoiesis

JOURNAL Cell 98 (5), 617-627 (1999)

PUBMED [10490101](#)

REFERENCE 7 (bases 1 to 2476)

AUTHORS Sasaki A, Yasukawa H, Suzuki A, Kamizono S, Syoda T, Kinjyo I, Sasaki M, Johnston JA and Yoshimura A.

TITLE Cytokine-inducible SH2 protein-3 (CIS3/SOCS3) inhibits Janus tyrosine kinase by binding through the N-terminal kinase inhibitory region as well as SH2 domain

JOURNAL Genes Cells 4 (6), 339-351 (1999)

PUBMED [10421843](#)

REFERENCE 8 (bases 1 to 2476)

AUTHORS Zhang JG, Farley A, Nicholson SE, Willson TA, Zugaro LM, Simpson RJ, Moritz RL, Cary D, Richardson R, Hausmann G, Kile BT, Kent SB, Alexander WS, Metcalf D, Hilton DJ, Nicola NA and Baca M.

TITLE The conserved SOCS box motif in suppressors of cytokine signaling binds to elongins B and C and may couple bound proteins to proteasomal degradation

JOURNAL Proc Natl Acad Sci U S A 96 (5), 2071-2076 (1999)

PUBMED [10051596](#)

REMARK Erratum:[Proc Natl Acad Sci U S A. 2015 Jun 2;112(22):E2979. Kile, B J [corrected to Kile, Benjamin T]. PMID: 25956176]

REFERENCE 9 (bases 1 to 2476)

AUTHORS Masuhara M, Sakamoto H, Matsumoto A, Suzuki R, Yasukawa H, Mitsui K, Wakioka T, Tanimura S, Sasaki A, Misawa H, Yokouchi M, Ohtsubo M and Yoshimura A.

TITLE Cloning and characterization of novel CIS family genes

JOURNAL Biochem Biophys Res Commun 239 (2), 439-446 (1997)

PUBMED [9344848](#)

REFERENCE 10 (bases 1 to 2476)

AUTHORS Minamoto S, Ikegami K, Ueno K, Narazaki M, Naka T, Yamamoto H, Matsumoto T, Saito H, Hosoe S and Kishimoto T.

TITLE Cloning and functional analysis of new members of STAT induced STAT inhibitor (SSI) family: SSI-2 and SSI-3

JOURNAL Biochem Biophys Res Commun 237 (1), 79-83 (1997)

PUBMED [9266833](#)

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [AC061992.11](#).

Summary: This gene encodes a member of the STAT-induced STAT inhibitor (SSI), also known as suppressor of cytokine signaling (SOCS), family. SSI family members are cytokine-inducible negative regulators of cytokine signaling. The expression of this gene is induced by various cytokines, including IL6, IL10, and interferon (IFN)-gamma. The protein encoded by this gene can bind to JAK2 kinase, and inhibit the activity of JAK2 kinase. Studies of the mouse counterpart of this gene suggested the roles of this gene in the negative regulation of fetal liver hematopoiesis, and placental development. [provided by RefSeq, Jul 2008].

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

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Homo sapiens coagulation factor III, tissue factor (F3), transcript variant 2, mRNA

NCBI Reference Sequence: NM_001178096.2

[FASTA Graphics](#)[Go to:](#)

LOCUS NM_001178096 2138 bp mRNA linear PRI 16-DEC-2020

DEFINITION Homo sapiens coagulation factor III, tissue factor (F3), transcript variant 2, mRNA.

ACCESSION NM_001178096

VERSION NM_001178096.2

KEYWORDS RefSeq.

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ORGANISM [Homo sapiens](#)

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 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2138)

AUTHORS Skendros P, Mitsios A, Chrysanthopoulou A, Mastellos DC, Metallidis

S, Rafailidis P, Ntinopoulou M, Sertaridou E, Tsironidou V,

Tsigalou C, Tektonidou M, Konstantinidis T, Papagoras C, Mitroulis
I, Germanidis G, Lambris JD and Ritis K.TITLE Complement and tissue factor-enriched neutrophil extracellular
traps are key drivers in COVID-19 immunothrombosis

JOURNAL J Clin Invest 130 (11), 6151-6157 (2020)

PUBMED [32759504](#)

REMARK GeneRIF: Complement and tissue factor-enriched neutrophil extracellular traps are key drivers in COVID-19 immunothrombosis.

REFERENCE 2 (bases 1 to 2138)

AUTHORS Hottz ED, Azevedo-Quintanilha IG, Palhinha L, Teixeira L, Barreto EA, Pao CRR, Righy C, Franco S, Souza TML, Kurtz P, Bozza FA and Bozza PT.

TITLE Platelet activation and platelet-monocyte aggregate formation trigger tissue factor expression in patients with severe COVID-19

JOURNAL Blood 136 (11), 1330-1341 (2020)

PUBMED [32678428](#)

REFERENCE 3 (bases 1 to 2138)

AUTHORS Luck K, Kim DK, Lambourne L, Spirohn K, Begg BE, Bian W, Brignall R, Cafarelli T, Campos-Laborie FJ, Charlotteaux B, Choi D, Cote AG, Daley M, Deimling S, Desbuleux A, Dricot A, Gebbia M, Hardy MF, Kishore N, Knapp JJ, Kovacs IA, Lemmens I, Mee MW, Mellor JC, Pollis C, Pons C, Richardson AD, Schlabach S, Teeking B, Yadav A, Babor M, Balcha D, Basha O, Bowman-Colin C, Chin SF, Choi SG, Colabella C, Coppin G, D'Amata C, De Ridder D, De Rouck S, Duran-Frigola M, Ennajdaoui H, Goebels F, Goehring L, Gopal A, Haddad G, Hatchi E, Helmy M, Jacob Y, Kassa Y, Landini S, Li R, van Lieshout N, MacWilliams A, Markey D, Paulson JN, Rangarajan S, Rasla J, Rayhan A, Rolland T, San-Miguel A, Shen Y, Sheykhharamli D, Sheynkman GM, Simonovsky E, Tasan M, Tejeda A, Tropepe V, Twizere JC, Wang Y, Weatheritt RJ, Weile J, Xia Y, Yang X, Yeger-Lotem E, Zhong Q, Aloy P, Bader GD, De Las Rivas J, Gaudet S, Hao T, Rak J, Tavernier J, Hill DE, Vidal M, Roth FP and Calderwood MA.

TITLE A reference map of the human binary protein interactome

JOURNAL Nature 580 (7803), 402-408 (2020)

PUBMED [32296183](#)

REFERENCE 4 (bases 1 to 2138)

AUTHORS Zioncheck TF, Roy S and Vehar GA.

TITLE The cytoplasmic domain of tissue factor is phosphorylated by a protein kinase C-dependent mechanism

JOURNAL J Biol Chem 267 (6), 3561-3564 (1992)

PUBMED [1740409](#)

REFERENCE 5 (bases 1 to 2138)

AUTHORS Broze GJ Jr, Girard TJ and Novotny WF.

TITLE Regulation of coagulation by a multivalent Kunitz-type inhibitor

JOURNAL Biochemistry 29 (33), 7539-7546 (1990)

PUBMED [2271516](#)

REMARK Review article

REFERENCE 6 (bases 1 to 2138)

AUTHORS Mackman N, Morrissey JH, Fowler B and Edgington TS.

TITLE Complete sequence of the human tissue factor gene, a highly regulated cellular receptor that initiates the coagulation protease cascade

JOURNAL Biochemistry 28 (4), 1755-1762 (1989)

PUBMED [2719931](#)

REFERENCE 7 (bases 1 to 2138)

AUTHORS Kao FT, Hartz J, Horton R, Nemerson Y and Carson SD.

TITLE Regional assignment of human tissue factor gene (F3) to chromosome 1p21-p22

JOURNAL Somat Cell Mol Genet 14 (4), 407-410 (1988)

PUBMED [3399965](#)

REFERENCE 8 (bases 1 to 2138)

AUTHORS Scarpati EM, Wen D, Broze GJ Jr, Miletich JP, Flandermeyer RR,
Siegel NR and Sadler JE.

TITLE Human tissue factor: cDNA sequence and chromosome localization of
the gene

JOURNAL Biochemistry 26 (17), 5234-5238 (1987)

PUBMED [2823875](#)

REFERENCE 9 (bases 1 to 2138)

AUTHORS Spicer,E.K., Horton,R., Bloem,L., Bach,R., Williams,K.R., Guha,A.,
Kraus,J., Lin,T.C., Nemerson,Y. and Konigsberg,W.H.

TITLE Isolation of cDNA clones coding for human tissue factor: primary
structure of the protein and cDNA

JOURNAL Proc Natl Acad Sci U S A 84 (15), 5148-5152 (1987)

PUBMED [3037536](#)

REFERENCE 10 (bases 1 to 2138)

AUTHORS Gouault-Helmann,M. and Josso,F.

TITLE [Initiation in vivo of blood coagulation. The role of white blood
cells and tissue factor (author's transl)]

JOURNAL Nouv Presse Med 8 (40), 3249-3253 (1979)

PUBMED [392457](#)

REMARK Review article

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The
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[AC093117.2](#).

On Aug 13, 2020 this sequence version replaced [NM_001178096.1](#).

Summary: This gene encodes coagulation factor III which is a cell surface glycoprotein. This factor enables cells to initiate the blood coagulation cascades, and it functions as the high-affinity receptor for the coagulation factor VII. The resulting complex provides a catalytic event that is responsible for initiation of the coagulation protease cascades by specific limited proteolysis. Unlike the other cofactors of these protease cascades, which circulate as nonfunctional precursors, this factor is a potent initiator that is fully functional when expressed on cell surfaces, for example, on monocytes. There are 3 distinct domains of this factor: extracellular, transmembrane, and cytoplasmic. Platelets and monocytes have been shown to express this coagulation factor under procoagulatory and proinflammatory stimuli, and a major role in HIV-associated coagulopathy has been described.

Platelet-dependent monocyte expression of coagulation factor III has been described to be associated with Coronavirus Disease 2019 (COVID-19) severity and mortality. This protein is the only one in the coagulation pathway for which a congenital deficiency has not been described. Alternate splicing results in multiple transcript variants.[provided by RefSeq, Aug 2020].

Transcript Variant: This variant (2) lacks an exon in the coding region, which results in a frameshift and an early stop codon, compared to variant 1. The encoded isoform (2) is shorter and has a distinct C-terminus, compared to 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.

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: AF497569.1, AF497570.1 [ECO:0000332]

##Evidence-Data-END##

##RefSeq-Attributes-START##

coronavirus related :: relevant for disease process

##RefSeq-Attributes-END##

COMPLETENESS: full length.

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853-2138	AC093117.2	14463-15748	c	
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ORIGIN

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 1681 tggatgttt
 1741 acaatctgttt
 1801 ataagacttt
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 1921 gtaatatt
 1981 gactggggat gtttacttgtt gtacttttttttttttttttttttttttttttttttttttttt
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Homo sapiens TNF superfamily member 14 (TNFSF14), transcript variant 2, mRNA
 NCBI Reference Sequence: NM_172014.3

FASTA GraphicsGo to:

LOCUS NM_172014 4406 bp mRNA linear PRI 13-DEC-2020
 DEFINITION Homo sapiens TNF superfamily member 14 (TNFSF14), transcript variant 2, mRNA.

ACCESSION NM_172014 XM_005259670

VERSION NM_172014.3

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4406)

AUTHORS Perlin DS, Zafir-Lavie I, Roadcap L, Raines S, Ware CF and Neil GA.

TITLE Levels of the TNF-Related Cytokine LIGHT Increase in Hospitalized COVID-19 Patients with Cytokine Release Syndrome and ARDS

JOURNAL mSphere 5 (4), e00699-20 (2020)

PUBMED [32817460](#)

REMARK GeneRIF: Levels of the TNF-Related Cytokine LIGHT Increase in Hospitalized COVID-19 Patients with Cytokine Release Syndrome and ARDS.

Publication Status: Online-Only

REFERENCE 2 (bases 1 to 4406)

AUTHORS Luck K, Kim DK, Lambourne L, Spirohn K, Begg BE, Bian W, Brignall R, Cafarelli T, Campos-Laborie FJ, Charlotteaux B, Choi D, Cote AG, Daley M, Deimling S, Desbuleux A, Dricot A, Gebbia M, Hardy MF, Kishore N, Knapp JJ, Kovacs IA, Lemmens I, Mee MW, Mellor JC, Pollis C, Pons C, Richardson AD, Schlabach S, Teeking B, Yadav A, Babor M, Balcha D, Basha O, Bowman-Colin C, Chin SF, Choi SG, Colabella C, Coppin G, D'Amata C, De Ridder D, De Rouck S, Duran-Frigola M, Ennajdaoui H, Goebels F, Goehring L, Gopal A, Haddad G, Hatchi E, Helmy M, Jacob Y, Kassa Y, Landini S, Li R, van Lieshout N, MacWilliams A, Markey D, Paulson JN, Rangarajan S, Rasla J, Rayhan A, Rolland T, San-Miguel A, Shen Y, Sheykharimli D, Sheynkman GM, Simonovsky E, Tasan M, Tejeda A, Tropepe V, Twizere JC, Wang Y, Weatheritt RJ, Weile J, Xia Y, Yang X, Yeger-Lotem E, Zhong Q, Aloy P, Bader GD, De Las Rivas J, Gaudet S, Hao T, Rak J, Tavernier J, Hill DE, Vidal M, Roth FP and Calderwood MA.

TITLE A reference map of the human binary protein interactome

JOURNAL Nature 580 (7803), 402-408 (2020)

PUBMED [32296183](#)

REFERENCE 3 (bases 1 to 4406)

AUTHORS Brunetti G, Storlino G, Oranger A, Colaianni G, Faienza MF, Ingravallo G, Di Comite M, Reseland JE, Celi M, Tarantino U, Passeri G, Ware CF, Grano M and Colucci S.

TITLE LIGHT/TNFSF14 regulates estrogen deficiency-induced bone loss

JOURNAL J Pathol 250 (4), 440-451 (2020)

PUBMED [31990039](#)

REMARK GeneRIF: TNFSF14 regulates estrogen deficiency-induced bone loss

REFERENCE 4 (bases 1 to 4406)

AUTHORS Iriyama T, Wang G, Yoshikawa M, Mimura N, Matsui H, Sayama S, Kumasawa K, Nagamatsu T, Koga K, Kotani T, Niimi K, Yamamoto E, Kellems RE, Xia Y, Osuga Y and Fujii T.

TITLE Increased LIGHT leading to sFlt-1 elevation underlies the

- pathogenic link between hydatidiform mole and preeclampsia
JOURNAL Sci Rep 9 (1), 10107 (2019)
PUBMED [31300808](#)
- REMARK GeneRIF: Increased LIGHT leading to sFlt-1 elevation underlies the pathogenic link between hydatidiform mole and preeclampsia.
Publication Status: Online-Only
- REFERENCE 5 (bases 1 to 4406)
AUTHORS Hsu CY, Tseng WK, Wu YW, Lin TH, Yeh HI, Chang KC, Wang JH, Chou RH, Huang CY, Huang PH, Leu HB, Yin WH, Wu CC, Lin SJ and Chen JW.
TITLE Circulating TNFSF14 (Tumor Necrosis Factor Superfamily 14) Predicts Clinical Outcome in Patients With Stable Coronary Artery Disease
JOURNAL Arterioscler Thromb Vasc Biol 39 (6), 1240-1252 (2019)
PUBMED [30943772](#)
- REMARK GeneRIF: Increased TNFSF14 levels were independently associated with the occurrence of cardiovascular events in patients with stable coronary artery disease.
- REFERENCE 6 (bases 1 to 4406)
AUTHORS Yu KY, Kwon B, Ni J, Zhai Y, Ebner R and Kwon BS.
TITLE A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis
JOURNAL J Biol Chem 274 (20), 13733-13736 (1999)
PUBMED [10318773](#)
- REFERENCE 7 (bases 1 to 4406)
AUTHORS Harrop JA, McDonnell PC, Brigham-Burke M, Lyn SD, Minton J, Tan KB, Dede K, Spamanato J, Silverman C, Hensley P, DiPrinzio R, Emery JG, Deen K, Eichman C, Chabot-Fletcher M, Truneh A and Young PR.
TITLE Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell growth
JOURNAL J Biol Chem 273 (42), 27548-27556 (1998)
PUBMED [9765287](#)
- REFERENCE 8 (bases 1 to 4406)
AUTHORS Zhai Y, Guo R, Hsu TL, Yu GL, Ni J, Kwon BS, Jiang GW, Lu J, Tan J, Ugustus M, Carter K, Rojas L, Zhu F, Lincoln C, Endress G, Xing L, Wang S, Oh KO, Gentz R, Ruben S, Lippman ME, Hsieh SL and Yang D.
TITLE LIGHT, a novel ligand for lymphotoxin beta receptor and TR2/HVEM induces apoptosis and suppresses in vivo tumor formation via gene transfer
JOURNAL J Clin Invest 102 (6), 1142-1151 (1998)
PUBMED [9739048](#)
- REFERENCE 9 (bases 1 to 4406)
AUTHORS Marsters SA, Sheridan JP, Pitti RM, Brush J, Goddard A and Ashkenazi A.
TITLE Identification of a ligand for the death-domain-containing receptor Apo3
JOURNAL Curr Biol 8 (9), 525-528 (1998)
PUBMED [9560343](#)
- REFERENCE 10 (bases 1 to 4406)
AUTHORS Mauri DN, Ebner R, Montgomery RI, Kochel KD, Cheung TC, Yu GL, Ruben S, Murphy M, Eisenberg RJ, Cohen GH, Spear PG and Ware CF.
TITLE LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are ligands for herpesvirus entry mediator
JOURNAL Immunity 8 (1), 21-30 (1998)
PUBMED [9462508](#)
- COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [AF064090.1](#), [AY028261.1](#),

[AC008760.7](#) and [AK026704.1](#).

On or before Apr 7, 2016 this sequence version replaced
[XM_005259670.2](#), [NM_172014.2](#).

Summary: The protein encoded by this gene is a member of the tumor necrosis factor (TNF) ligand family. This protein is a ligand for TNFRSF14, which is a member of the tumor necrosis factor receptor superfamily, and which is also known as a herpesvirus entry mediator (HVEM). This protein may function as a costimulatory factor for the activation of lymphoid cells and as a deterrent to infection by herpesvirus. This protein has been shown to stimulate the proliferation of T cells, and trigger apoptosis of various tumor cells. This protein is also reported to prevent tumor necrosis factor alpha mediated apoptosis in primary hepatocyte. Two alternatively spliced transcript variant encoding distinct isoforms have been reported. [provided by RefSeq, Jul 2008].

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.

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: SRR1163658.48979.1, AY028261.1
[ECO:0000332]
RNAseq introns :: single sample supports all introns
SAMEA2142586, SAMEA2144333
[ECO:0000348]

##Evidence-Data-END##

COMPLETENESS: complete on the 3' end.

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2616-4091	AK026704.1	442-1917		
4092-4268	AC008760.7	97048-97224	c	
4269-4406	AK026704.1	2095-2232		
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Homo sapiens troponin I1, slow skeletal type (TNNI1), mRNA

NCBI Reference Sequence: NM_003281.4

[FASTA Graphics](#)

[Go to:](#)

LOCUS NM_003281 6110 bp mRNA linear PRI 13-OCT-2020

DEFINITION Homo sapiens troponin I1, slow skeletal type (TNNI1), mRNA.

ACCESSION NM_003281

VERSION NM_003281.4

KEYWORDS RefSeq; MANE Select.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 6110)

AUTHORS Nie SF, Yu M, Xie T, Yang F, Wang HB, Wang ZH, Li M, Gao XL, Lv BJ,
Wang SJ, Zhang XB, He SL, Qiu ZH, Liao YH, Zhou ZH and Cheng X.

TITLE Cardiac Troponin I Is an Independent Predictor for Mortality in
Hospitalized Patients With COVID-19

JOURNAL Circulation 142 (6), 608-610 (2020)

PUBMED [32539541](#)

REMARK GeneRIF: Cardiac Troponin I Is an Independent Predictor for
Mortality in Hospitalized Patients With COVID-19.

REFERENCE 2 (bases 1 to 6110)

AUTHORS Luck K, Kim DK, Lambourne L, Spirohn K, Begg BE, Bian W, Brignall
R, Cafarelli T, Campos-Laborie FJ, Charlotteaux B, Choi D, Cote AG,

Daley M, Deimling S, Desbuleux A, Dricot A, Gebbia M, Hardy MF,

Kishore N, Knapp JJ, Kovacs IA, Lemmens I, Mee MW, Mellor JC,

Pollis C, Pons C, Richardson AD, Schlabach S, Teeking B, Yadav A,

Babor M, Balcha D, Basha O, Bowman-Colin C, Chin SF, Choi SG,

Colabella C, Coppin G, D'Amata C, De Ridder D, De Rouck S,

Duran-Frigola M, Ennajdaoui H, Goebels F, Goehring L, Gopal A,

Haddad G, Hatchi E, Helmy M, Jacob Y, Kassa Y, Landini S, Li R, van

Lieshout N, MacWilliams A, Markey D, Paulson JN, Rangarajan S,

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D, Sheynkman GM, Simonovsky E, Tasan M, Tejeda A, Tropepe V,

Twizere JC, Wang Y, Weatheritt RJ, Weile J, Xia Y, Yang X,

- Yeger-Lotem E, Zhong Q, Aloy P, Bader GD, De Las Rivas J, Gaudet S, Hao T, Rak J, Tavernier J, Hill DE, Vidal M, Roth FP and Calderwood MA.
- TITLE A reference map of the human binary protein interactome
JOURNAL Nature 580 (7803), 402-408 (2020)
PUBMED [32296183](#)
- REFERENCE 3 (bases 1 to 6110)
AUTHORS de Almeida Thiengo D, Strogoff-de-Matos JP, Lugon JR and Graciano ML.
- TITLE Troponin I at admission in the intensive care unit predicts the need of dialysis in septic patients
JOURNAL BMC Nephrol 19 (1), 329 (2018)
PUBMED [30453890](#)
- REMARK GeneRIF: Troponin I levels at intensive care unit admission are a strong independent predictor of dialysis needs in sepsis.
Publication Status: Online-Only
- REFERENCE 4 (bases 1 to 6110)
AUTHORS Kaess BM, de Las Heras Gala T, Zierer A, Meisinger C, Wahl S, Peters A, Todd J, Herder C, Huth C, Thorand B and Koenig W.
- TITLE Ultra-sensitive troponin I is an independent predictor of incident coronary heart disease in the general population
JOURNAL Eur J Epidemiol 32 (7), 583-591 (2017)
PUBMED [28585121](#)
- REMARK GeneRIF: Ultrasensitive troponin I was detectable in almost all individuals of a study sample reflecting middle-aged to elderly European general population. Ultrasensitive troponin concentrations exhibit an independent, graded, positive relation with incident CHD [coronary heart disease].
- REFERENCE 5 (bases 1 to 6110)
AUTHORS Shafi A, Siddiqui N, Imtiaz S and Din Sajid MU.
- TITLE Left Ventricular Systolic Dysfunction Predicted By Early Troponin I Release After Anthracycline Based Chemotherapy In Breast Cancer Patients
JOURNAL J Ayub Med Coll Abbottabad 29 (2), 266-269 (2017)
PUBMED [28718245](#)
- REMARK GeneRIF: Studied use of serum levels of Troponin I as a predictive biomarker for diagnosis of left ventricular systolic dysfunction after anthracycline treatment in breast cancer.
- REFERENCE 6 (bases 1 to 6110)
AUTHORS Corin SJ, Juhasz O, Zhu L, Conley P, Kedes L and Wade R.
- TITLE Structure and expression of the human slow twitch skeletal muscle troponin I gene
JOURNAL J Biol Chem 269 (14), 10651-10659 (1994)
PUBMED [8144655](#)
- REFERENCE 7 (bases 1 to 6110)
AUTHORS Bhavsar PK, Dhoot GK, Cumming DV, Butler-Browne GS, Yacoub MH and Barton PJ.
- TITLE Developmental expression of troponin I isoforms in fetal human heart
JOURNAL FEBS Lett 292 (1-2), 5-8 (1991)
PUBMED [1959627](#)
- REFERENCE 8 (bases 1 to 6110)
AUTHORS Hunkeler NM, Kullman J and Murphy AM.
- TITLE Troponin I isoform expression in human heart
JOURNAL Circ Res 69 (5), 1409-1414 (1991)
PUBMED [1934363](#)

REFERENCE 9 (bases 1 to 6110)

AUTHORS Wade R, Eddy R, Shows TB and Kedes L.

TITLE cDNA sequence, tissue-specific expression, and chromosomal mapping of the human slow-twitch skeletal muscle isoform of troponin I

JOURNAL Genomics 7 (3), 346-357 (1990)

PUBMED [2365354](#)

REFERENCE 10 (bases 1 to 6110)

AUTHORS Suzuki H, Kawarabayasi Y, Kondo J, Abe T, Nishikawa K, Kimura S, Hashimoto T and Yamamoto T.

TITLE Structure and regulation of rat long-chain acyl-CoA synthetase

JOURNAL J Biol Chem 265 (15), 8681-8685 (1990)

PUBMED [2341402](#)

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [BC012600.1](#), [AC096677.2](#) and [AL832006.2](#).

This sequence is a reference standard in the [RefSeqGene](#) project.

On Nov 22, 2018 this sequence version replaced [NM_003281.3](#).

Summary: Troponin proteins associate with tropomyosin and regulate the calcium sensitivity of the myofibril contractile apparatus of striated muscles. Troponin I (TnI), along with troponin T (TnT) and troponin C (TnC), is one of 3 subunits that form the troponin complex of the thin filaments of striated muscle. TnI is the inhibitory subunit; blocking actin-myosin interactions and thereby mediating striated muscle relaxation. The TnI subfamily contains three genes: TnI-skeletal-fast-twitch, TnI-skeletal-slow-twitch, and TnI-cardiac. The TnI-fast and TnI-slow genes are expressed in fast-twitch and slow-twitch skeletal muscle fibers, respectively, while the TnI-cardiac gene is expressed exclusively in cardiac muscle tissue. This gene encodes the Troponin-I-skeletal-slow-twitch protein. This gene is expressed in cardiac and skeletal muscle during early development but is restricted to slow-twitch skeletal muscle fibers in adults. The encoded protein prevents muscle contraction by inhibiting calcium-mediated conformational changes in actin-myosin complexes. [provided by RefSeq, Jul 2008].

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: AL831975.1, BX510903.2 [ECO:0000332]

RNAseq introns :: single sample supports all introns

SAMEA2162946, SAMN03267751
[ECO:0000348]

##Evidence-Data-END##

##RefSeq-Attributes-START##

MANE Ensembl match :: ENST00000361379.9/ENSP00000354488.4

RefSeq Select criteria :: based on single protein-coding transcript

##RefSeq-Attributes-END##

COMPLETENESS: full length.

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Homo sapiens solute carrier family 6 member 20 (SLC6A20), transcript variant 1, mRNA

NCBI Reference Sequence: NM_020208.4

[FASTA Graphics](#)[Go to:](#)

LOCUS NM_020208 5425 bp mRNA linear PRI 12-DEC-2020

DEFINITION Homo sapiens solute carrier family 6 member 20 (SLC6A20), transcript variant 1, mRNA.

ACCESSION NM_020208

VERSION NM_020208.4

KEYWORDS RefSeq; MANE Select.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5425)

AUTHORS Ellinghaus D, Degenhardt F, Bujanda L, Buti M, Albillos A, Invernizzi P, Fernandez J, Prati D, Baselli G, Asselta R, Grimsrud MM, Milani C, Aziz F, Kassens J, May S, Wendorff M, Wienbrandt L, Uellendahl-Werth F, Zheng T, Yi X, de Pablo R, Chercoles AG, Palom A, Garcia-Fernandez AE, Rodriguez-Frias F, Zanella A, Bandera A, Protti A, Aghemo A, Lleo A, Biondi A, Caballero-Garralda A, Gori A, Tanck A, Carreras Nolla A, Latiano A, Fracanzani AL, Peschuck A, Julia A, Pesenti A, Voza A, Jimenez D, Mateos B, Nafria Jimenez B, Quereda C, Paccapelo C, Gassner C, Angelini C, Cea C, Solier A, Pestana D, Muniz-Diaz E, Sandoval E, Paraboschi EM, Navas E, Garcia Sanchez F, Ceriotti F, Martinelli-Boneschi F, Peyvandi F, Blasi F, Tellez L, Blanco-Grau A, Hemmrich-Stanisak G, Grasselli G, Costantino G, Cardamone G, Foti G, Aneli S, Kurihara H, ElAbd H, My I, Galvan-Femenia I, Martin J, Erdmann J, Ferrusquia-Acosta J, Garcia-Etxabarria K, Izquierdo-Sanchez L, Bettini LR, Sumoy L, Terranova L, Moreira L, Santoro L, Scudeller L, Mesonero F, Roade L, Ruhlemann MC, Schaefer M, Carrabba M, Riveiro-Barciela M, Figuera Basso ME, Valsecchi MG, Hernandez-Tejero M, Acosta-Herrera M, D'Angio M, Baldini M, Cazzaniga M, Schulzky M, Ceconi M, Wittig M, Ciccarelli M, Rodriguez-Gandia M, Bocciolone M, Miozzo M, Montano N, Braun N, Sacchi N, Martinez N, Ozer O, Palmieri O, Faverio P, Preatoni P, Bonfanti P, Omodei P, Tentorio P, Castro P, Rodrigues PM, Blandino Ortiz A, de Cid R, Ferrer R, Gualtierotti R, Nieto R, Goerg S, Badalamenti S, Marsal S, Matullo G, Pelusi S, Juzenas S, Aliberti S, Monzani V, Moreno V, Wesse T, Lenz TL, Pumarola T, Rimoldi V, Bosari S, Albrecht W, Peter W, Romero-Gomez M, D'Amato M, Duga S, Banales JM, Hov JR, Folseraas T, Valenti L, Franke A and Karlsen TH.

CONSRM Severe Covid-19 GWAS Group

TITLE Genomewide Association Study of Severe Covid-19 with Respiratory Failure

JOURNAL N Engl J Med 383 (16), 1522-1534 (2020)

PUBMED [32558485](#)

REFERENCE 2 (bases 1 to 5425)

AUTHORS Xie X, He Q, Huang L, Li L, Yao Y, Xia H, Zhao J, Zhong W and Zhang

Y.

TITLE Associations of SLC6A20 genetic polymorphisms with Hirschsprung's disease in a Southern Chinese population

JOURNAL Biosci Rep 39 (8) (2019)

PUBMED [31358688](#)

REMARK GeneRIF: Associations of SLC6A20 genetic polymorphisms with Hirschsprung's disease in a Southern Chinese population.

Publication Status: Online-Only

REFERENCE 3 (bases 1 to 5425)

AUTHORS Sweeney MD, Zhao Z, Montagne A, Nelson AR and Zlokovic BV.

TITLE Blood-Brain Barrier: From Physiology to Disease and Back

JOURNAL Physiol Rev 99 (1), 21-78 (2019)

PUBMED [30280653](#)

REMARK Review article

REFERENCE 4 (bases 1 to 5425)

AUTHORS Meier C, Camargo SM, Hunziker S, Moehrlen U, Gros SJ, Bode P, Leu S, Meuli M, Holland-Cunz S, Verrey F and Vuille-Dit-Bille RN.

TITLE Intestinal IMINO transporter SIT1 is not expressed in human newborns

JOURNAL Am J Physiol Gastrointest Liver Physiol 315 (5), G887-G895 (2018)

PUBMED [30160974](#)

REMARK GeneRIF: SIT1 is not expressed in small intestine of human newborns.

REFERENCE 5 (bases 1 to 5425)

AUTHORS Lee JS, Oh JT, Kim JH, Seo JM, Kim DY, Park KW, Kim HY, Jung K, Park BL, Koh I and Shin HD.

TITLE Association Analysis of SLC6A20 Polymorphisms With Hirschsprung Disease

JOURNAL J Pediatr Gastroenterol Nutr 62 (1), 64-70 (2016)

PUBMED [26049783](#)

REMARK GeneRIF: Imputed meta-analysis revealed that 13 SLC6A20 SNPs were significantly associated with Hirschsprung disease. In further subgroup analysis, SLC6A20 polymorphisms appeared to have increased associations with Long-Segment Hirschsprung disease.

REFERENCE 6 (bases 1 to 5425)

AUTHORS Vuille-dit-Bille RN, Camargo SM, Emmenegger L, Sasse T, Kummer E, Jando J, Hamie QM, Meier CF, Hunziker S, Forras-Kaufmann Z, Kuyumcu S, Fox M, Schwizer W, Fried M, Lindenmeyer M, Gotze O and Verrey F.

TITLE Human intestine luminal ACE2 and amino acid transporter expression increased by ACE-inhibitors

JOURNAL Amino Acids 47 (4), 693-705 (2015)

PUBMED [25534429](#)

REMARK GeneRIF: SIT1, B(0)AT1 and ACE2 were co-localized in the brush-border membrane of small intestine enterocytes.

REFERENCE 7 (bases 1 to 5425)

AUTHORS Kanei-Ishii C, Nomura T, Tanikawa J, Ichikawa-Iwata E and Ishii S.

TITLE Differential sensitivity of v-Myb and c-Myb to Wnt-1-induced protein degradation

JOURNAL J Biol Chem 279 (43), 44582-44589 (2004)

PUBMED [15308626](#)

REFERENCE 8 (bases 1 to 5425)

AUTHORS Kiss H, Kedra D, Kiss C, Kost-Alimova M, Yang Y, Klein G, Imreh S and Dumanski JP.

TITLE The LZTFL1 gene is a part of a transcriptional map covering 250 kb within the common eliminated region 1 (C3CER1) in 3p21.3

JOURNAL Genomics 73 (1), 10-19 (2001)

PUBMED [11352561](#)

REFERENCE 9 (bases 1 to 5425)

AUTHORS Nash SR, Giros B, Kingsmore SF, Kim KM, el-Mestikawy S, Dong Q, Fumagalli F, Seldin MF and Caron MG.

TITLE Cloning, gene structure and genomic localization of an orphan transporter from mouse kidney with six alternatively-spliced isoforms

JOURNAL Recept Channels 6 (2), 113-128 (1998)

PUBMED [9932288](#)

REFERENCE 10 (bases 1 to 5425)

AUTHORS Stevens,B.R. and Wright,E.M.

TITLE Kinetics of the intestinal brush border proline (Imino) carrier

JOURNAL J Biol Chem 262 (14), 6546-6551 (1987)

PUBMED [3571270](#)

REMARK GeneRIF: Characterization and substrate specificity of the Na⁺ coupled IMINO transport system in apical brush border membranes of epithelial cells. Identically found in kidney proximal tubule.

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [DR006419.1](#), [AJ276207.1](#), [AC098476.2](#) and [EL949345.1](#).

This sequence is a reference standard in the [RefSeqGene](#) project.

On Nov 23, 2018 this sequence version replaced [NM_020208.3](#).

Summary: Transport of small hydrophilic substances across cell membranes is mediated by substrate-specific transporter proteins which have been classified into several families of related genes. The protein encoded by this gene belongs to the sodium:neurotransmitter symporter (SNF) family and functions as a proline transporter expressed in kidney and small intestine. Mutations in this gene are associated with Hyperglycinuria and Iminoglycinuria. [provided by RefSeq, Jul 2020].

Transcript Variant: This variant (1) encodes isoform 1.

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: AJ276207.1, BC126197.1 [ECO:0000332]

RNAseq introns :: single sample supports all introns

SAMEA2144835 [ECO:0000348]

##Evidence-Data-END##

##RefSeq-Attributes-START##

MANE Ensembl match :: ENST00000358525.9/ENSP00000346298.4

RefSeq Select criteria :: based on conservation, expression

##RefSeq-Attributes-END##

COMPLETENESS: full length.

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Homo sapiens FYVE and coiled-coil domain autophagy adaptor 1 (FYCO1), transcript variant 10, mRNA

NCBI Reference Sequence: NM_001386421.1

[FASTA Graphics](#)[Go to:](#)

LOCUS NM_001386421 8598 bp mRNA linear PRI 17-DEC-2020

DEFINITION Homo sapiens FYVE and coiled-coil domain autophagy adaptor 1

(FYCO1), transcript variant 10, mRNA.

ACCESSION NM_001386421 XM_011534111

VERSION NM_001386421.1

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 8598)

AUTHORS Ellinghaus D, Degenhardt F, Bujanda L, Buti M, Albillos A, Invernizzi P, Fernandez J, Prati D, Baselli G, Asselta R, Grimsrud MM, Milani C, Aziz F, Kassens J, May S, Wendorff M, Wienbrandt L, Uellendahl-Werth F, Zheng T, Yi X, de Pablo R, Chercoles AG, Palom A, Garcia-Fernandez AE, Rodriguez-Frias F, Zanella A, Bandera A, Protti A, Aghemo A, Lleo A, Biondi A, Caballero-Garralda A, Gori A, Tanck A, Carreras Nolla A, Latiano A, Fracanzani AL, Peschuck A, Julia A, Pesenti A, Voza A, Jimenez D, Mateos B, Nafria Jimenez B, Quereda C, Paccapelo C, Gassner C, Angelini C, Cea C, Solier A, Pestana D, Muniz-Diaz E, Sandoval E, Paraboschi EM, Navas E, Garcia Sanchez F, Ceriotti F, Martinelli-Boneschi F, Peyvandi F, Blasi F, Tellez L, Blanco-Grau A, Hemmrich-Stanisak G, Grasselli G, Costantino G, Cardamone G, Foti G, Aneli S, Kurihara H, ElAbd H, My I, Galvan-Femenia I, Martin J, Erdmann J, Ferrusquia-Acosta J, Garcia-Etxebarria K, Izquierdo-Sanchez L, Bettini LR, Sumoy L, Terranova L, Moreira L, Santoro L, Scudeller L, Mesonero F, Roade L, Ruhlemann MC, Schaefer M, Carrabba M, Riveiro-Barciela M, Figuera Basso ME, Valsecchi MG, Hernandez-Tejero M, Acosta-Herrera M, D'Angio M, Baldini M, Cazzaniga M, Schulzky M, Cecconi M, Wittig M, Ciccarelli M, Rodriguez-Gandia M, Bocciolone M, Miozzo M, Montano N, Braun N, Sacchi N, Martinez N, Ozer O, Palmieri O, Faverio P, Pretoni P, Bonfanti P, Omodei P, Tentorio P, Castro P, Rodrigues PM, Blandino Ortiz A, de Cid R, Ferrer R, Gualtierotti R, Nieto R, Goerg S, Badalamenti S, Marsal S, Matullo G, Pelusi S, Juzenas S, Aliberti S, Monzani V, Moreno V, Wesse T, Lenz TL, Pumarola T, Rimoldi V, Bosari S, Albrecht W, Peter W, Romero-Gomez M, D'Amato M, Duga S, Banales JM, Hov JR, Folseraas T, Valenti L, Franke A and Karlsen TH.

CONSRTM Severe Covid-19 GWAS Group

TITLE Genomewide Association Study of Severe Covid-19 with Respiratory Failure

JOURNAL N Engl J Med 383 (16), 1522-1534 (2020)

PUBMED [32558485](#)

REFERENCE 2 (bases 1 to 8598)

AUTHORS Sakurai S, Shimizu T and Ohto U.

TITLE Crystal structure of the FYCO1 RUN domain suggests possible interfaces with small GTPases

JOURNAL Acta Crystallogr F Struct Biol Commun 76 (Pt 8), 326-333 (2020)

PUBMED [32744243](#)

REFERENCE 3 (bases 1 to 8598)

AUTHORS Thavarajah T, Dos Santos CC, Slutsky AS, Marshall JC, Bowden P, Romaschin A and Marshall JG.

TITLE The plasma peptides of sepsis

JOURNAL Clin Proteomics 17, 26 (2020)

PUBMED [32636717](#)

REMARK Publication Status: Online-Only

REFERENCE 4 (bases 1 to 8598)

AUTHORS Iqbal H, Khan SY, Zhou L, Irum B, Ali M, Ahmed MR, Shahzad M, Ali MH, Naeem MA, Riazuddin S, Hejtmancik JF and Riazuddin SA.

TITLE Mutations in FYCO1 identified in families with congenital cataracts

JOURNAL Mol Vis 26, 334-344 (2020)

PUBMED [32355443](#)

REMARK Publication Status: Online-Only

REFERENCE 5 (bases 1 to 8598)

AUTHORS Rothwell S, Lilleker JB and Lamb JA.
TITLE Genetics in inclusion body myositis
JOURNAL Curr Opin Rheumatol 29 (6), 639-644 (2017)
PUBMED [28777108](#)
REMARK Review article
REFERENCE 6 (bases 1 to 8598)
AUTHORS Chen J, Ma Z, Jiao X, Fariss R, Kantorow WL, Kantorow M, Pras E, Frydman M, Pras E, Riazuddin S, Riazuddin SA and Hejtmancik JF.
TITLE Mutations in FYCO1 cause autosomal-recessive congenital cataracts
JOURNAL Am J Hum Genet 88 (6), 827-838 (2011)
PUBMED [21636066](#)
REMARK GeneRIF: FYCO1 is involved in lens development and transparency in humans, and mutations in this gene are one of the most common causes of autosomal-recessive congenital cataracts in the Pakistani population.
REFERENCE 7 (bases 1 to 8598)
AUTHORS Pankiv S and Johansen T.
TITLE FYCO1: linking autophagosomes to microtubule plus end-directing molecular motors
JOURNAL Autophagy 6 (4), 550-552 (2010)
PUBMED [20364109](#)
REFERENCE 8 (bases 1 to 8598)
AUTHORS Pankiv S, Alemu EA, Brech A, Bruun JA, Lamark T, Overvatn A, Bjorkoy G and Johansen T.
TITLE FYCO1 is a Rab7 effector that binds to LC3 and PI3P to mediate microtubule plus end-directed vesicle transport
JOURNAL J Cell Biol 188 (2), 253-269 (2010)
PUBMED [20100911](#)
REMARK GeneRIF: We have characterized the LC3-, Rab7-, and phosphatidylinositol-3-phosphate-binding domains in FYCO1 and mapped part of the CC region essential for MT plus end-directed transport.
REFERENCE 9 (bases 1 to 8598)
AUTHORS Ghosh D, Lippert D, Krokhin O, Cortens JP and Wilkins JA.
TITLE Defining the membrane proteome of NK cells
JOURNAL J Mass Spectrom 45 (1), 1-25 (2010)
PUBMED [19946888](#)
REFERENCE 10 (bases 1 to 8598)
AUTHORS Kiss H, Yang Y, Kiss C, Andersson K, Klein G, Imreh S and Dumanski JP.
TITLE The transcriptional map of the common eliminated region 1 (C3CER1) in 3p21.3
JOURNAL Eur J Hum Genet 10 (1), 52-61 (2002)
PUBMED [11896456](#)
REMARK GeneRIF: Maps to a region of chromosome 3p21.3 which is frequently deleted in tumors.
COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [AC099782.2](#).
On Aug 25, 2020 this sequence version replaced [XM_011534111.3](#).

Summary: The gene encodes a Rab7 adapter protein that is implicated in the microtubule transport of autophagosomes. The encoded protein contains a RUN domain, a FYVE-type zinc finger domain, and Golgi dynamics (GOLD) domain. The encoded protein plays a role in microtubule plus end-directed transport of autophagic vesicles through interactions with the small GTPase Rab7,

phosphatidylinositol-3-phosphate (PI3P), the autophagosome marker LC3, and the kinesin KIF5. Mutations in this gene are associated with inclusion body myositis (IBM) and autosomal recessive congenital cataracts (CATC2). [provided by RefSeq, Aug 2020].

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: SRR7346977.2471468.1,
DRR138518.449027.1 [ECO:0000332]

##Evidence-Data-END##

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588-694	AC099782.2	161164-161270	c	
695-838	AC099782.2	159013-159156	c	
839-929	AC099782.2	155600-155690	c	
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3357-3449	AC099782.2	150958-151050	c	
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Mutant Severe acute respiratory syndrome coronavirus 2 clone SARS-CoV-2-MA10, complete genome

GenBank: MT952602.1

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LOCUS MT952602 29882 bp RNA linear SYN 19-OCT-2020

DEFINITION Mutant Severe acute respiratory syndrome coronavirus 2 clone
SARS-CoV-2-MA10, complete genome.

ACCESSION MT952602

VERSION MT952602.1

KEYWORDS

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ORGANISM [Severe acute respiratory syndrome coronavirus 2](#)

Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes;
Nidovirales; Cornidovirinae; Coronaviridae; Orthocoronavirinae;
Betacoronavirus; Sarbecovirus.

REFERENCE 1 (bases 1 to 29882)

AUTHORS Leist,S.R., Dinnon,K.H. III, Schafer,A., Tse,L.V., Okuda,K.,
Hou,Y.J., West,A., Edwards,C.E., Sanders,W., Fritch,E.J.,
Gully,K.L., Scobey,T., Brown,A.J., Sheahan,T.P., Moorman,N.J.,
Boucher,R.C., Gralinski,L.E., Montgomery,S.A. and Baric,R.S.

TITLE A Mouse-Adapted SARS-CoV-2 Induces Acute Lung Injury and Mortality
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AUTHORS Leist,S.R., Dinnon,K.H. III, Schafer,A., Tse,L.V., Okuda,K.,
Hou,Y.J., West,A., Edwards,C.E., Sanders,W., Fritch,E.J.,
Gully,K.L., Scobey,T., Brown,A.J., Sheahan,T.P., Moorman,N.J.,
Boucher,R.C., Gralinski,L.E., Montgomery,S.A. and Baric,R.S.

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JOURNAL Submitted (31-AUG-2020) Epidemiology, University of North Carolina
at Chapel Hill, 2107 McGavran-Greenberg CB7435, Chapel Hill, NC
27599, USA

COMMENT ##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing
##Assembly-Data-END##

FEATURES Location/Qualifiers

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