Sequence insulin preprotein pada genome manusia (Chromosome 11) memiliki 2 exon yang dibatasi 1 intron. Gen insulin preprotein memiliki Panjang coding sequence 330 bp (diawali start codon AUG dan diakhiri stop codon UAG) dengan total amino acid sequence insulin preprotein ada 110 asam amino.

Untuk mengisolasi fragment gen insulin preprotein perlu dilakukan dengan RT-PCR (Reverse Transcriptase PCR). Template yang digunakan adalah total RNA/mRNA dari darah manusia. Primer yang digunakan adalah primer forward pada posisi start codon, dan primer reverse pada posisi stop codon. Tolong dibaca tentang RT PCR.

Homo sapiens chromosome 11, GRCh38.p13 Primary Assembly

NCBI Reference Sequence: NC\_000011.10

FASTA Graphics

LOCUS NC\_000011 1431 bp DNA linear CON 17-AUG-2020

DEFINITION Homo sapiens chromosome 11, GRCh38.p13 Primary Assembly.

ACCESSION NC\_000011 REGION: complement(2159779..2161209)

VERSION NC\_000011.10

DBLINK BioProject: PRJNA168

Assembly: GCF\_000001405.39

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 1431)

AUTHORS Taylor,T.D., Noguchi,H., Totoki,Y., Toyoda,A., Kuroki,Y., Dewar,K.,

Lloyd,C., Itoh,T., Takeda,T., Kim,D.W., She,X., Barlow,K.F.,

Bloom,T., Bruford,E., Chang,J.L., Cuomo,C.A., Eichler,E.,

FitzGerald,M.G., Jaffe,D.B., LaButti,K., Nicol,R., Park,H.S.,

Seaman,C., Sougnez,C., Yang,X., Zimmer,A.R., Zody,M.C.,

Birren,B.W., Nusbaum,C., Fujiyama,A., Hattori,M., Rogers,J.,

Lander,E.S. and Sakaki,Y.

TITLE Human chromosome 11 DNA sequence and analysis including novel gene

identification

JOURNAL Nature 440 (7083), 497-500 (2006)

PUBMED 16554811

REFERENCE 2 (bases 1 to 1431)

CONSRTM International Human Genome Sequencing Consortium

TITLE Finishing the euchromatic sequence of the human genome

JOURNAL Nature 431 (7011), 931-945 (2004)

PUBMED 15496913

REFERENCE 3 (bases 1 to 1431)

AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C.,

Baldwin,J., Devon,K., Dewar,K., Doyle,M., FitzHugh,W., Funke,R.,

Gage,D., Harris,K., Heaford,A., Howland,J., Kann,L., Lehoczky,J.,

LeVine,R., McEwan,P., McKernan,K., Meldrim,J., Mesirov,J.P.,

Miranda,C., Morris,W., Naylor,J., Raymond,C., Rosetti,M.,

Santos,R., Sheridan,A., Sougnez,C., Stange-Thomann,N.,

Stojanovic,N., Subramanian,A., Wyman,D., Rogers,J., Sulston,J.,

Ainscough,R., Beck,S., Bentley,D., Burton,J., Clee,C., Carter,N.,

Coulson,A., Deadman,R., Deloukas,P., Dunham,A., Dunham,I.,

Durbin,R., French,L., Grafham,D., Gregory,S., Hubbard,T.,

Humphray,S., Hunt,A., Jones,M., Lloyd,C., McMurray,A., Matthews,L.,

Mercer,S., Milne,S., Mullikin,J.C., Mungall,A., Plumb,R., Ross,M.,

Shownkeen,R., Sims,S., Waterston,R.H., Wilson,R.K., Hillier,L.W.,

McPherson,J.D., Marra,M.A., Mardis,E.R., Fulton,L.A.,

Chinwalla,A.T., Pepin,K.H., Gish,W.R., Chissoe,S.L., Wendl,M.C.,

Delehaunty,K.D., Miner,T.L., Delehaunty,A., Kramer,J.B., Cook,L.L.,

Fulton,R.S., Johnson,D.L., Minx,P.J., Clifton,S.W., Hawkins,T.,

Branscomb,E., Predki,P., Richardson,P., Wenning,S., Slezak,T.,

Doggett,N., Cheng,J.F., Olsen,A., Lucas,S., Elkin,C.,

Uberbacher,E., Frazier,M., Gibbs,R.A., Muzny,D.M., Scherer,S.E.,

Bouck,J.B., Sodergren,E.J., Worley,K.C., Rives,C.M., Gorrell,J.H.,

Metzker,M.L., Naylor,S.L., Kucherlapati,R.S., Nelson,D.L.,

Weinstock,G.M., Sakaki,Y., Fujiyama,A., Hattori,M., Yada,T.,

Toyoda,A., Itoh,T., Kawagoe,C., Watanabe,H., Totoki,Y., Taylor,T.,

Weissenbach,J., Heilig,R., Saurin,W., Artiguenave,F., Brottier,P.,

Bruls,T., Pelletier,E., Robert,C., Wincker,P., Smith,D.R.,

Doucette-Stamm,L., Rubenfield,M., Weinstock,K., Lee,H.M.,

Dubois,J., Rosenthal,A., Platzer,M., Nyakatura,G., Taudien,S.,

Rump,A., Yang,H., Yu,J., Wang,J., Huang,G., Gu,J., Hood,L.,

Rowen,L., Madan,A., Qin,S., Davis,R.W., Federspiel,N.A.,

Abola,A.P., Proctor,M.J., Myers,R.M., Schmutz,J., Dickson,M.,

Grimwood,J., Cox,D.R., Olson,M.V., Kaul,R., Raymond,C., Shimizu,N.,

Kawasaki,K., Minoshima,S., Evans,G.A., Athanasiou,M., Schultz,R.,

Roe,B.A., Chen,F., Pan,H., Ramser,J., Lehrach,H., Reinhardt,R.,

McCombie,W.R., de la Bastide,M., Dedhia,N., Blocker,H.,

Hornischer,K., Nordsiek,G., Agarwala,R., Aravind,L., Bailey,J.A.,

Bateman,A., Batzoglou,S., Birney,E., Bork,P., Brown,D.G.,

Burge,C.B., Cerutti,L., Chen,H.C., Church,D., Clamp,M.,

Copley,R.R., Doerks,T., Eddy,S.R., Eichler,E.E., Furey,T.S.,

Galagan,J., Gilbert,J.G., Harmon,C., Hayashizaki,Y., Haussler,D.,

Hermjakob,H., Hokamp,K., Jang,W., Johnson,L.S., Jones,T.A.,

Kasif,S., Kaspryzk,A., Kennedy,S., Kent,W.J., Kitts,P.,

Koonin,E.V., Korf,I., Kulp,D., Lancet,D., Lowe,T.M., McLysaght,A.,

Mikkelsen,T., Moran,J.V., Mulder,N., Pollara,V.J., Ponting,C.P.,

Schuler,G., Schultz,J., Slater,G., Smit,A.F., Stupka,E.,

Szustakowski,J., Thierry-Mieg,D., Thierry-Mieg,J., Wagner,L.,

Wallis,J., Wheeler,R., Williams,A., Wolf,Y.I., Wolfe,K.H.,

Yang,S.P., Yeh,R.F., Collins,F., Guyer,M.S., Peterson,J.,

Felsenfeld,A., Wetterstrand,K.A., Patrinos,A., Morgan,M.J., de

Jong,P., Catanese,J.J., Osoegawa,K., Shizuya,H., Choi,S. and

Chen,Y.J.

CONSRTM International Human Genome Sequencing Consortium

TITLE Initial sequencing and analysis of the human genome

JOURNAL Nature 409 (6822), 860-921 (2001)

PUBMED 11237011

REMARK Erratum:[Nature 2001 Aug 2;412(6846):565]

COMMENT REFSEQ INFORMATION: The reference sequence is identical to

CM000673.2.

On Feb 3, 2014 this sequence version replaced NC\_000011.9.

Assembly Name: GRCh38.p13 Primary Assembly

The DNA sequence is composed of genomic sequence, primarily

finished clones that were sequenced as part of the Human Genome

Project. PCR products and WGS shotgun sequence have been added

where necessary to fill gaps or correct errors. All such additions

are manually curated by GRC staff. For more information see:

https://genomereference.org.

##Genome-Annotation-Data-START##

Annotation Provider :: NCBI

Annotation Status :: Updated annotation

Annotation Name :: Homo sapiens Updated Annotation

Release 109.20200815

Annotation Version :: 109.20200815

Annotation Pipeline :: NCBI eukaryotic genome annotation

pipeline

Annotation Software Version :: 8.5

Annotation Method :: Best-placed RefSeq; propagated

RefSeq model

Features Annotated :: Gene; mRNA; CDS; ncRNA

##Genome-Annotation-Data-END##

FEATURES Location/Qualifiers

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/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="11"

gene 1..>1431

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/gene\_synonym="INSIGF"

/note="INS-IGF2 readthrough; Derived by automated

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/db\_xref="HGNC:HGNC:33527"

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/note="Derived by automated computational analysis using

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gene prediction method: BestRefSeq."

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/db\_xref="GeneID:723961"

/db\_xref="HGNC:HGNC:33527"

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SRQFRQRALGTSDSPVLFIHCPGAAGTAQGLEYRGRRVTTELVWEEVDSSPQPQGSES

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gene 1..1431

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/note="insulin; Derived by automated computational

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/db\_xref="GeneID:3630"

/db\_xref="HGNC:HGNC:6081"

/db\_xref="MIM:176730"

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PNDM4"

/product="insulin, transcript variant 1"

/note="Derived by automated computational analysis using

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/transcript\_id="NM\_000207.3"

/db\_xref="Ensembl:ENST00000381330.5"

/db\_xref="GeneID:3630"

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/gene\_synonym="IDDM; IDDM1; IDDM2; ILPR; IRDN; MODY10;

PNDM4"

/product="insulin, transcript variant 2"

/note="Derived by automated computational analysis using

gene prediction method: BestRefSeq."

/transcript\_id="NM\_001185097.2"

/db\_xref="GeneID:3630"

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YQLENYCN"

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gene prediction method: BestRefSeq."

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YQLENYCN"

CDS join(239..425,1213..1358) Posisi exons. Ada 2 exon.

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gene prediction method: BestRefSeq."

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YQLENYCN" Urutan asam amino

ORIGIN

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181 cacctggcct tcagcctgcc tcagccctgc ctgtctccca gatcactgtc cttctgccat

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721 caccctcatt tgatgaccgc agattcaagt gttttgttaa gtaaagtcct gggtgacctg

781 gggtcacagg gtgccccacg ctgcctgcct ctgggcgaac accccatcac gcccggagga

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1201 acgtcctggc agtggggcag gtggagctgg gcgggggccc tggtgcaggc agcctgcagc

1261 ccttggccct ggaggggtcc ctgcagaagc gtggcattgt ggaacaatgc tgtaccagca

1321 tctgctccct ctaccagctg gagaactact gcaactagac gcagcccgca ggcagcccca

1381 cacccgccgc ctcctgcacc gagagagatg gaataaagcc cttgaaccag c

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Translate dengan <http://bio.lundberg.gu.se/edu/translat.html>

N = Coding sequence/mRNA sequence

N = asam amino sequence

N = intron

1 AGCCCUCCAGGACAGGCUGCAUCAGAAGAGGCCAUCAAGCAGGUCUGUUCCAAGGGCCUU 60

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A L Q D R L H Q K R P S S R S V P R A F

P S R T G C I R R G H Q A G L F Q G P L

61 UGCGUCAGGUGGGCUCAGGAUUCCAGGGUGGCUGGACCCCAGGCCCCAGCUCUGCAGCAG 120

C V R W A Q D S R V A G P Q A P A L Q Q

A S G G L R I P G W L D P R P Q L C S R

R Q V G S G F Q G G W T P G P S S A A G

121 GGAGGACGUGGCUGGGCUCGUGAAGCAUGUGGGGGUGAGCCCAGGGGCCCCAAGGCAGGG 180

G G R G W A R E A C G G E P R G P K A G

E D V A G L V K H V G V S P G A P R Q G

R T W L G S \* S M W G \* A Q G P Q G R A

181 CACCUGGCCUUCAGCCUGCCUCAGCCCUGCCUGUCUCCCAGAUCACUGUCCUUCUGCCAU 240

H L A F S L P Q P C L S P R S L S F C H

T W P S A C L S P A C L P D H C P S A M

P G L Q P A S A L P V S Q I T V L L P W

241 GGCCCUGUGGAUGCGCCUCCUGCCCCUGCUGGCGCUGCUGGCCCUCUGGGGACCUGACCC 300

G P V D A P P A P A G A A G P L G T \* P

A L W M R L L P L L A L L A L W G P D P

P C G C A S C P C W R C W P S G D L T Q

301 AGCCGCAGCCUUUGUGAACCAACACCUGUGCGGCUCACACCUGGUGGAAGCUCUCUACCU 360

S R S L C E P T P V R L T P G G S S L P

A A A F V N Q H L C G S H L V E A L Y L

P Q P L \* T N T C A A H T W W K L S T \*

361 AGUGUGCGGGGAACGAGGCUUCUUCUACACACCCAAGACCCGCCGGGAGGCAGAGGACCU 420

S V R G T R L L L H T Q D P P G G R G P

V C G E R G F F Y T P K T R R E A E D L

C A G N E A S S T H P R P A G R Q R T C

421 GCAGGGUGAGCCAACUGCCCAUUGCUGCCCCUGGCCGCCCCCAGCCACCCCCUGCUCCUG 480

A G \* A N C P L L P L A A P S H P L L L

Q G E P T A H C C P W P P P A T P C S W

R V S Q L P I A A P G R P Q P P P A P G

481 GCGCUCCCACCCAGCAUGGGCAGAAGGGGGCAGGAGGCUGCCACCCAGCAGGGGGUCAGG 540

A L P P S M G R R G Q E A A T Q Q G V R

R S H P A W A E G G R R L P P S R G S G

A P T Q H G Q K G A G G C H P A G G Q V

541 UGCACUUUUUUAAAAAGAAGUUCUCUUGGUCACGUCCUAAAAGUGACCAGCUCCCUGUGG 600

C T F L K R S S L G H V L K V T S S L W

A L F \* K E V L L V T S \* K \* P A P C G

H F F K K K F S W S R P K S D Q L P V A

601 CCCAGUCAGAAUCUCAGCCUGAGGACGGUGUUGGCUUCGGCAGCCCCGAGAUACAUCAGA 660

P S Q N L S L R T V L A S A A P R Y I R

P V R I S A \* G R C W L R Q P R D T S E

Q S E S Q P E D G V G F G S P E I H Q R

661 GGGUGGGCACGCUCCUCCCUCCACUCGCCCCUCAAACAAAUGCCCCGCAGCCCAUUUCUC 720

G W A R S S L H S P L K Q M P R S P F L

G G H A P P S T R P S N K C P A A H F S

V G T L L P P L A P Q T N A P Q P I S P

721 CACCCUCAUUUGAUGACCGCAGAUUCAAGUGUUUUGUUAAGUAAAGUCCUGGGUGACCUG 780

H P H L M T A D S S V L L S K V L G D L

T L I \* \* P Q I Q V F C \* V K S W V T W

P S F D D R R F K C F V K \* S P G \* P G

781 GGGUCACAGGGUGCCCCACGCUGCCUGCCUCUGGGCGAACACCCCAUCACGCCCGGAGGA 840

G S Q G A P R C L P L G E H P I T P G G

G H R V P H A A C L W A N T P S R P E E

V T G C P T L P A S G R T P H H A R R R

841 GGGCGUGGCUGCCUGCCUGAGUGGGCCAGACCCCUGUCGCCAGGCCUCACGGCAGCUCCA 900

G R G C L P E W A R P L S P G L T A A P

G V A A C L S G P D P C R Q A S R Q L H

A W L P A \* V G Q T P V A R P H G S S I

901 UAGUCAGGAGAUGGGGAAGAUGCUGGGGACAGGCCCUGGGGAGAAGUACUGGGAUCACCU 960

\* S G D G E D A G D R P W G E V L G S P

S Q E M G K M L G T G P G E K Y W D H L

V R R W G R C W G Q A L G R S T G I T C

961 GUUCAGGCUCCCACUGUGACGCUGCCCCGGGGCGGGGGAAGGAGGUGGGACAUGUGGGCG 1020

V Q A P T V T L P R G G G R R W D M W A

F R L P L \* R C P G A G E G G G T C G R

S G S H C D A A P G R G K E V G H V G V

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L G P V G P H P V W V T L P L T W V Q P

W G L \* V H T Q C G \* P S L \* P G S S P

G A C R S T P S V G D P P S N L G P A R

1081 GGCUGGAGAUGGGUGGGAGUGCGACCUAGGGCUGGCGGGCAGGCGGGCACUGUGUCUCCC 1140

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A G D G W E C D L G L A G R R A L C L P

L E M G G S A T \* G W R A G G H C V S L

1141 UGACUGUGUCCUCCUGUGUCCCUCUGCCUCGCCGCUGUUCCGGAACCUGCUCUGCGCGGC 1200

\* L C P P V S L C L A A V P E P A L R G

D C V L L C P S A S P L F R N L L C A A

T V S S C V P L P R R C S G T C S A R H

1201 ACGUCCUGGCAGUGGGGCAGGUGGAGCUGGGCGGGGGCCCUGGUGCAGGCAGCCUGCAGC 1260

T S W Q W G R W S W A G A L V Q A A C S

R P G S G A G G A G R G P W C R Q P A A

V L A V G Q V E L G G G P G A G S L Q P

1261 CCUUGGCCCUGGAGGGGUCCCUGCAGAAGCGUGGCAUUGUGGAACAAUGCUGUACCAGCA 1320

P W P W R G P C R S V A L W N N A V P A

L G P G G V P A E A W H C G T M L Y Q H

L A L E G S L Q K R G I V E Q C C T S I

1321 UCUGCUCCCUCUACCAGCUGGAGAACUACUGCAACUAGACGCAGCCCGCAGGCAGCCCCA 1380

S A P S T S W R T T A T R R S P Q A A P

L L P L P A G E L L Q L D A A R R Q P H

C S L Y Q L E N Y C N \* T Q P A G S P T

1381 CACCCGCCGCCUCCUGCACCGAGAGAGAUGGAAUAAAGCCCUUGAACCAGC 1431

H P P P P A P R E M E \* S P \* T S

T R R L L H R E R W N K A L E P

P A A S C T E R D G I K P L N Q