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تقریباً ۶۸۷۰۰۰۰۰ نتیجه (۰٫۳۶ ثانیه)

ترجمه این صفحه ■ <https://www.ncbi.nlm.nih.gov>

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23 Feb 2023

Ever wonder who is behind all the data at the National Center for Biotechnology Information (NCBI)? Who is developing

Now Available! More Mammalian Cross-Species Alignments in the Comparative Genome Viewer (CGV)

MMAB metabolism of cobalamin associated B [*Homo sapiens* (human)]

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Gene ID: 326625, updated on 4-Dec-2022

Summary

Official Symbol MMAB provided by [HGNC](#)

Official Full Name metabolism of cobalamin associated B provided by [HGNC](#)

Primary source [HGNC:HGNC:19331](#)

See related [Ensembl:ENSG00000139428](#) [MIM:607568](#); [AllianceGenome:HGNC:19331](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Homo sapiens](#)

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

Also known as ATR; cob; cblB; CFAP23

Summary This gene encodes a protein that catalyzes the final step in the conversion of vitamin B(12) into adenosylcobalamin (AdoCbl), a vitamin B12-containing coenzyme for methylmalonyl-CoA mutase. Mutations in the gene are the cause of vitamin B12-dependent methylmalonic aciduria linked to the cblB complementation group. Alternatively spliced transcript variants have been found. [provided by RefSeq, Apr 2011]

Expression Ubiquitous expression in liver (RPKM 6.8), adrenal (RPKM 5.6) and 25 other tissues [See more](#)

Orthologs [mouse](#) [all](#)

NEW Try the new [Gene table](#)

Try the new [Transcript table](#)

Genomic context

Location: 12q24.11

See MMAB in [Genome Data Viewer](#)

Exon count: 14

Annotation release	Status	Assembly	Chr	Location
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[Interactions](#)

[General gene information](#)

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Genome Browsers

[Genome Data Viewer](#)

[Variation Viewer \(GRCh37.p13\)](#)

[Variation Viewer \(GRCh38\)](#)

[1000 Genomes Browser \(GRCh37.p13\)](#)

[Ensembl](#)

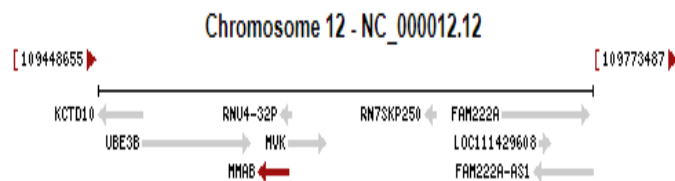
Genomic context

Location: 12q24.11

See MMAB in [Genome Data Viewer](#)

Exon count: 14

Annotation release	Status	Assembly	Chr	Location
110	current	GRCh38.p14 (GCF_000001405.40)	12	NC_000012.12 (109553715..109573504, complement)
110	current	T2T-CHM13v2.0 (GCF_009914755.1)	12	NC_060936.1 (109528617..109548403, complement)
105.20220307	previous assembly	GRCh37.p13 (GCF_000001405.25)	12	NC_000012.11 (109991520..110011309, complement)



Genome Browsers

[Genome Data Viewer](#)

[Variation Viewer \(GRCh37.p13\)](#)

[Variation Viewer \(GRCh38\)](#)

[1000 Genomes Browser \(GRCh37.p13\)](#)

[Ensembl](#)

[UCSC](#)

Related information

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[3D structures](#)

[BioAssay by Target \(List\)](#)

[BioAssay, by Gene target](#)

XP_011836571.1

EC [2.5.1.17](#)

XP_047284726.1

EC [2.5.1.17](#)

X v ^

1/1

NG_

NCBI Reference Sequences (RefSeq)

NEW Try the new [Transcript table](#)

RefSeqs maintained independently of Annotated Genomes

These reference sequences exist independently of genome builds. [Explain](#)

Genomic

1. [NG_007096.1](#) RefSeqGene

Range	4994..24783
Download	GenBank , FASTA , Sequence Viewer (Graphics)

mRNA and Protein(s)

1. [NM_052845.4](#) → [NP_443077.1](#) corrinoid adenosyltransferase MMAB precursor

[See identical proteins and their annotated locations for NP_443077.1](#)

Status: REVIEWED

Description	Transcript Variant: This variant (1) encodes a functional protein.
Source sequence(s)	AC007570 , BC011831 , BI497024 , DA718661
Consensus CDS	CCDS9131.1
UniProtKB/Swiss-Prot	Q96EY8 , Q9BSH0
Related	ENSP00000445920.1 , ENST00000545712.7

Conserved Domains (1) [summary](#)

Homo sapiens metabolism of cobalamin associated B (MMAB), RefSeqGene on chromosome 12

NCBI Reference Sequence: [NG_007096.1](#)[FASTA](#) [Graphics](#)[Go to:](#)

LOCUS NG_007096 19790 bp DNA linear PRI 02-JAN-2023
DEFINITION Homo sapiens metabolism of cobalamin associated B (MMAB),
RefSeqGene on chromosome 12.
ACCESSION [NG_007096](#) REGION: 4994..24783
VERSION NG_007096.1
KEYWORDS RefSeq; RefSeqGene.
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 19790)
AUTHORS Dobson CM, Wai T, Leclerc D, Kadir H, Narang M, Lerner-Ellis JP,
Hudson TJ, Rosenblatt DS and Gravel RA.
TITLE Identification of the gene responsible for the cblB complementation
group of vitamin B12-dependent methylmalonic aciduria
JOURNAL Hum Mol Genet 11 (26), 3361-3369 (2002)
PUBMED [12471062](#)
REFERENCE 2 (bases 1 to 19790)
AUTHORS Manoli,I., Sloan,J.L. and Venditti,C.P.
TITLE Isolated Methylmalonic Acidemia
JOURNAL (in) Adam MP, Everman DB, Mirzaa GM, Pagon RA, Wallace SE, Bean
LJH, Gripp KW and Amemiya A (Eds.);
GENEREVIEWS(R);
(1993)
PUBMED [20301409](#)
REFERENCE 3 (bases 1 to 19790)

Change region shown

- Whole sequence
 Selected region

from: to:

Customize view

Analyze this sequence

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Related information

[Protein](#)[PubMed](#)[Taxonomy](#)[Components \(Core\)](#)[Full text in PMC](#)[Gene](#)[HomoloGene](#)[OMIM](#)[PubMed \(Weighted\)](#)

Homo sapiens metabolism of cobalamin associated B (MMAB), RefSeqGene on chromosome 12

NCBI Reference Sequence: NG_007096.1

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

LOCUS NG_007096 19790 bp DNA linear PRI 02-JAN-2023

DEFINITION Homo sapiens metabolism of cobalamin associated B (MMAB),
RefSeqGene on chromosome 12.ACCESSION [NG_007096](#) REGION: 4994..24783

VERSION NG_007096.1

KEYWORDS RefSeq; RefSeqGene.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrh
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 19790)

AUTHORS Dobson CM, Wai T, Leclerc D, Kadir H, Narang M, Lerner-E
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LJH, Gripp KW and Amemiya A (Eds.);GENEREVIEWS(R);
(1993)PUBMED [20301409](#)

REFERENCE 3 (bases 1 to 19790)

Opens the Highlight Feature Bar and highlights feature annotations from the FEATURES table of the record. The Highlight Feature Bar can be used to navigate to and highlight other features and provides links to display the highlighted region separately. Links in the FEATURES table will also highlight the corresponding region of the sequence. [More...](#)

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 Whole sequence Selected regionfrom: to:

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Change region shown



Customize view



Analyze this sequence



Run BLAST

Pick Primers

Homo sapiens metabolism of cobalamin associated B (MMAB), RefSeqGene on chromosome 12

NCBI Reference Sequence: NG_007096.1

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

LOCUS NG_007096 25048 bp DNA linear PRI 02-JAN-2023

DEFINITION Homo sapiens metabolism of cobalamin associated B (MMAB),
RefSeqGene on chromosome 12.

ACCESSION NG_007096

VERSION NG_007096.1

KEYWORDS RefSeq; RefSeqGene.

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 25048)

AUTHORS Dobson CM, Wai T, Leclerc D, Kadir H, Narang M, Lerner-Ellis JP,
Hudson TJ, Rosenblatt DS and Gravel RA.TITLE Identification of the gene responsible for the cblB complementation
group of vitamin B12-dependent methylmalonic aciduria

JOURNAL Hum Mol Genet 11 (26), 3361-3369 (2002)

PubMed [12471062](#)

FEATURES 2 (bases 1 to 25048)

SOURCE Manoli, I., Sloan, J.L. and Venditti, C.P.

TITLE Isolated Methylmalonic Acidemia

JOURNAL (in) Adam MP, Everman DB, Mirzaa GM, Pagon RA, Wallace SE, Bean
LJH, Gripp KW and Amemiya A (Eds.);
GENEREVIEWS(R);
(1993)

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- misc_RNA
- mRNA
- transit_peptide

CDS [Feature](#) 1 of 8 NG_007096 : 2 segments (minus strand)

[Details](#)Display: [FASTA](#) [GenBank](#) [Help](#)

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Homo sapiens metabolism of cobalamin associated B (MMAB), RefSeqGene on chromosome 12

NCBI Reference Sequence: NG_007096.1

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DEFINITION Homo sapiens metabolism of cobalamin associated B (MMAB),
RefSeqGene on chromosome 12.
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VERSION NG_007096.1
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SOURCE Homo sapiens (human)
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AUTHORS Dobson CM, Wai T, Leclerc D, Kadir H, Narang M, Lerner-Ellis JP,

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Homo sapiens metabolism of cobalamin associated B (MMAB), RefSeqGene on chromosome 12

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Homo sapiens metabolism of cobalamin associated B (MMAB), RefSeqGene on chromosome 12

NCBI Reference Sequence: NG_007096.1

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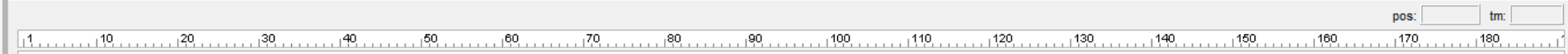
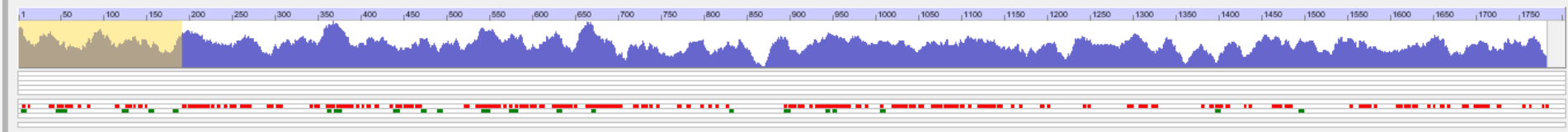
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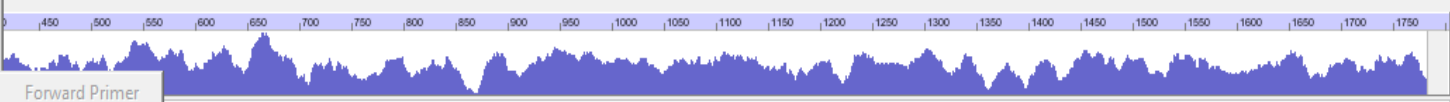


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- Key Info
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- Hairpin Formation
- Composition & Tm
- False Priming Sites
- Homology
- Selected Oligonucleotides
- Oligonucleotide Sets
- PCR
- LCR
- Melting Temperature Graph
- Internal Stability
- Sequence Frequency
- Open Reading Frames
- Restriction Enzyme Sites
- Restriction Enzyme Sites in Protein
- Hybridization Time
- Concentrations
- All Checked Ctrl+X

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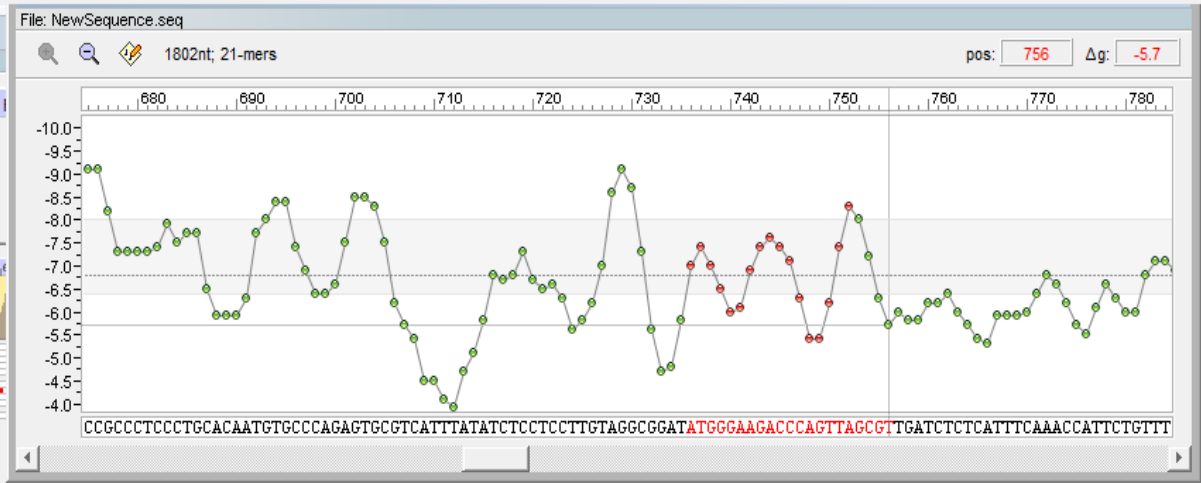
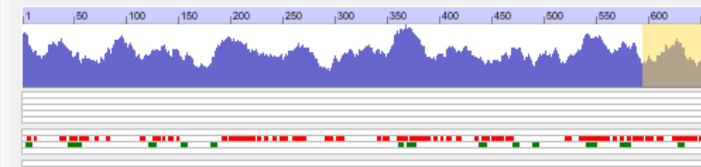
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t_m :	60.6°C	<input checked="" type="checkbox"/> PCR Product	[---,---] nt		



pos: tm:
600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780

ATGGGAAGACCCAGTTAGCGT
CTTGACACTGGAGTAGAGTCTTGGCATTACAGCAGTGCCCTCGTGTGCCATCCATTAAGTGCAAGATGGCTGGGCCCCGCCCTCCCTGCACAATGTGCCAGAGTGCGTCATTTATATCTCCTCCTTGTAGGGGATATGGGAAGACCCAGTTAGCGTTGATCTCTCATTTCAAACCATTCTGTITT
GAACTGTGACCTCATCTCAGGAACCGTAAGTGTCTGTCGACCCGGAGCACACGGTAGGTAATTCACGTTCTACCGACCCGGGGGGGAGGGACGTGTTACACGGGTCTCACGCAGTAAATATAGAGGAGGAACATCCGCCTATACCCCTTCTGGGTCAATCGCAACTAGAGAGTAAGTTGGTAAGACAAA

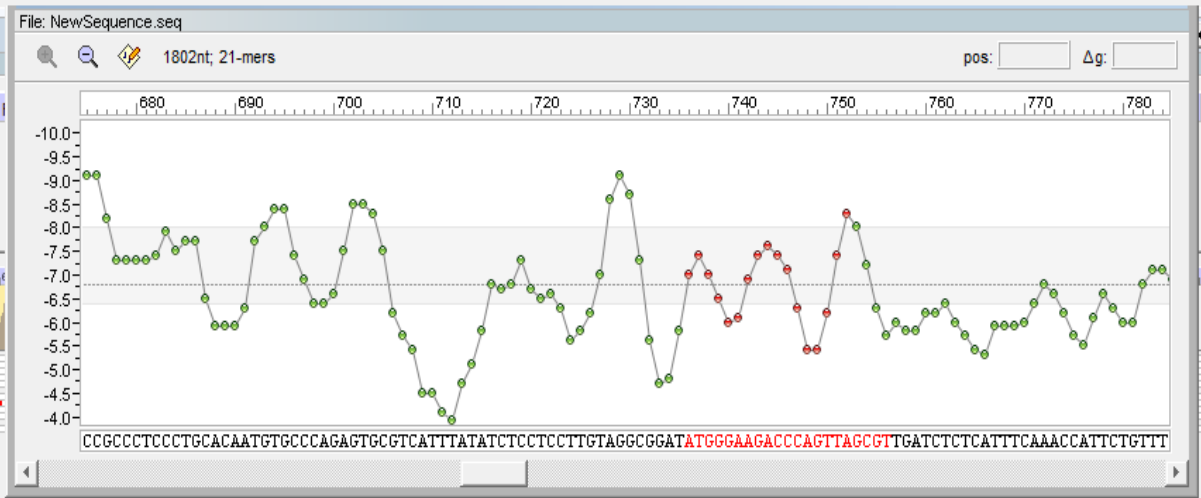
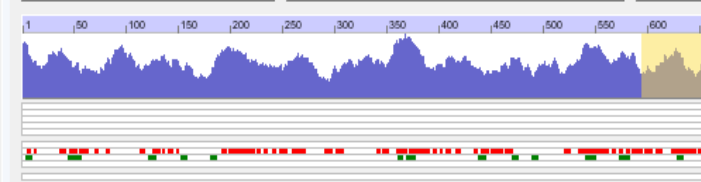
L D T G V E S L A F T A A G L V C H P L S A R W L G P R P P C T M C P E C V I Y I S S L - A D M G R P S - R - S L I S N H S V C



Sequence

File: NewSequence.seq

DNA Sequence	Selected Oligo	Position	Length	#
Sequence Length: 1802 nt	<input checked="" type="checkbox"/> Forward Primer	736	21	
Reading Frame: +1	<input type="checkbox"/> Reverse Primer	---	---	
Current Oligo Length: 21 nt	<input type="checkbox"/> Upper Oligo	---	---	
Position: 736	<input type="checkbox"/> Lower Oligo	---	---	
t_m : 60.6°C	<input checked="" type="checkbox"/> PCR Product	[---,---] nt		



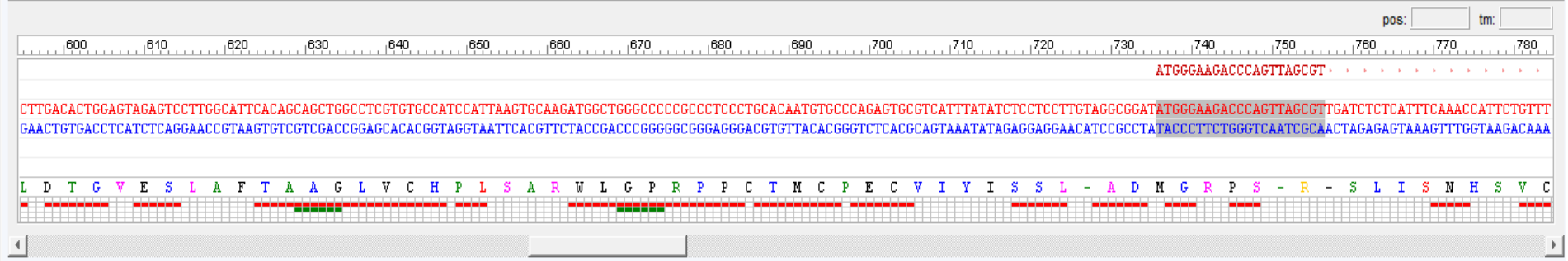
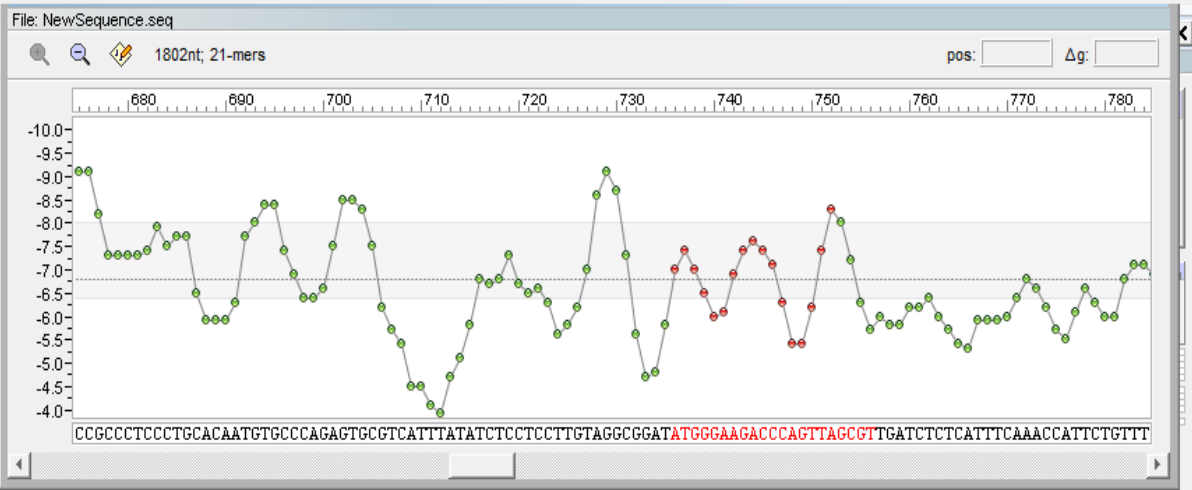
pos: tm:

ATGGGAAGACCCAGTTAGCGT

CTTGACACTGGAGTAGAGTCTTGGCATTACAGCAGCTGGCCTCGTGTCCATCCATTAAGTGAAGATGGCTGGGCCCCGCCCTCCTGCACAATGTGCCAGAGTGCCTCATTATATCTCCTCCTTGTAGGGGATATGGGAAGACCCAGTTAGCGTTGATCTCTCATTTCAAACATTCTGTTT
GAACTGTGACCTCATCTCAGGAACCGTAAGTGTCTGCAGCCGGAGCACAGGTAGGTAATTCACGTTTACCCGACCCGGGGGGGGAGGACGTTTACACGGGTCTCAGCAGTAAATATAGAGGAGGAACATCCGCTATACCTTCTGGGTCAATCGCAACTAGAGAGTAAAGTTTGGTAAGACAAA

L D T G V E S L A F T A A G L V C H P L S A R W L G P R P P C T M C P E C V I Y I S S L - A D M G R P S - R - S L I S N H S V C

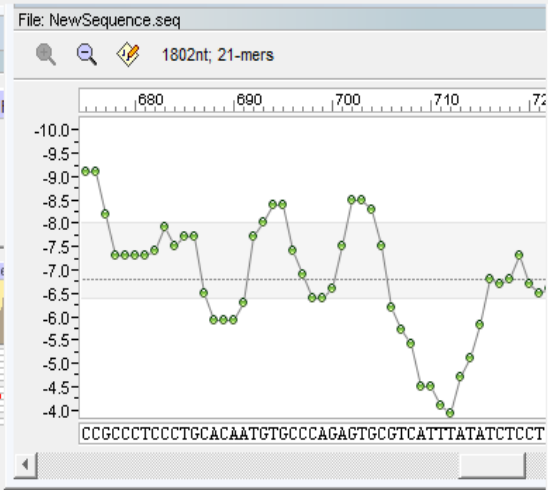
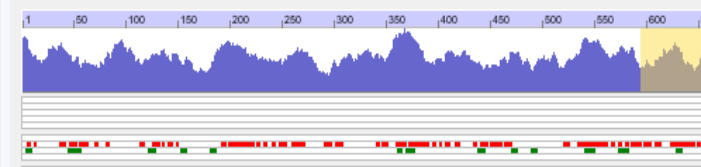
- Key Info
- Duplex Formation**
 - Forward Primer
 - Reverse Primer
 - Upper Oligo
 - Lower Oligo
 - Current Oligo
 - Mixed Oligos
- Hairpin Formation
- Composition & Tm
- False Priming Sites
- Homology
- Selected Oligonucleotides
- Oligonucleotide Sets
- PCR
- LCR
- Melting Temperature Graph
- Internal Stability
- Sequence Frequency
- Open Reading Frames
- Restriction Enzyme Sites
- Restriction Enzyme Sites in Protein
- Hybridization Time
- Concentrations
- All Checked Ctrl+X





Sequence
File: NewSequence.seq

DNA Sequence	Selected Oligo	Position	Length	#
Sequence Length: 1802 nt	<input checked="" type="checkbox"/> Forward Primer	736	21	
Reading Frame: +1	<input type="checkbox"/> Reverse Primer	---	---	
Current Oligo Length: 21 nt	<input type="checkbox"/> Upper Oligo	---	---	
Position: 736	<input type="checkbox"/> Lower Oligo	---	---	
T_m : 60.6°C	<input checked="" type="checkbox"/> PCR Product	[---,---] nt		



File: NewSequence.seq
Forward Primer NewSequence:736F21

The most stable 3'-dimer: # of hydrogen bonds = 2; $\Delta G = -0.3$ kcal/mol

```

5' ATGGGAAGACCCAGTTAGCGT 3'
      |||
3' TCGGATTGACCCAGAAAGGTA 5'
    
```

The most stable dimer overall: # of hydrogen bonds = 8; $\Delta G = -8.6$ kcal/mol; $T_m = 7.4^\circ\text{C}$

```

5' ATGGGAAGACCCAGTTAGCGT 3'
      |||
3' TCGGATTGACCCAGAAAGGTA 5'
    
```

Hairpin: loop = 4 nt; $\Delta G = -1.6$ kcal/mol; $T_m = 51.8^\circ\text{C}$

```

5' ATGGGAA-
      |||
3' TCGGATTGACCCAG-
    
```

600 610 620 630 640 650 660 670 680 690 700 710

CTTGACACTGGAGTAGAGTCTTGGCATTACACAGAGCTGGCCCTCGTGTGCCATCCATTAAGTGCAAGATGGCTGGGCCCCGCCCTCCCTGCACAATGTGCCAGAGTGGCTCATTATATCTCTCTCTTGTAGCCGGATATGGGAAGACCCAGTTAGCGTTGATCTCTCATTTCAAACCATTCTGTTT
 GAACTGTGACCTCATCTCAGGAACCGTAAGTGTCTGTCGACCGGAGCACACGGTAGGTAATTCACGTTTACCCGACCCGGGGGGGGAGGAGCGTGTACACGGTCTTCACGCAAGTAATATAGAGGAGGAACATCCGCTATACCCCTTCTGGGTCAATCGCAACTAGAGAGTAAAGTTGGTAAGACAAA

L D T G V E S L A F T A A G L V C H P L S A R W L G P R P P C T M C P E C V I Y I S S L - A D M G R P S - R - S L I S N H S V C

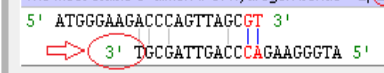


Forward Primer Duplexes

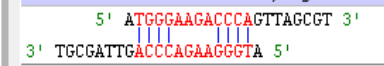
File: NewSequence.seq

Forward Primer NewSequence:736F21

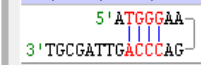
The most stable 3'-dimer: # of hydrogen bonds = 2, $\Delta G = -0.3$ kcal/mol



The most stable dimer overall: # of hydrogen bonds = 8, $\Delta G = -8.6$ kcal/mol, $T_m = 7.4^\circ\text{C}$



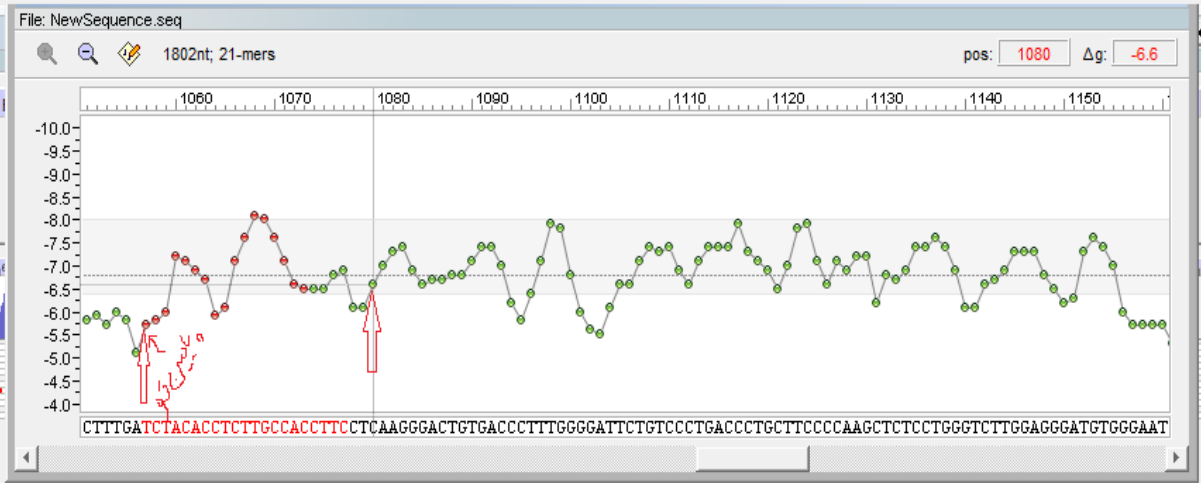
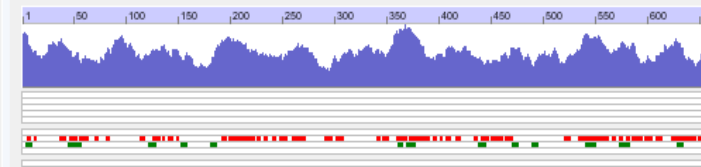
Hairpin: loop = 4 nt, $\Delta G = -1.6$ kcal/mol, $T_m = 51.8^\circ\text{C}$





Sequence
File: NewSequence.seq

DNA Sequence	Selected Oligo	Position	Length	#
Sequence Length: 1802 nt	<input checked="" type="checkbox"/> Forward Primer	736	21	
Reading Frame: +1	<input checked="" type="checkbox"/> Reverse Primer	1057	24	
Current Oligo Length: 21 nt	<input type="checkbox"/> Upper Oligo	---	---	
Position: 1057	<input type="checkbox"/> Lower Oligo	---	---	
t_m : 58.6°C	<input checked="" type="checkbox"/> PCR Product	[345,---] nt		



pos: tm:

980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150

GAGGAGCTTGGCCCTTCTGGGGTCTGGTTCCTGAAGAGCTCACCCAGAGAGGCTCAAAGCAGCCTTTTGTCCAGCTCAGCTTTGATCTACACCTCTGCCACCTTCCTCAAGGGACTGTGACCCCTTTGGGGATTCTGTCCCTGACCCTGCTTCCCCAAGCTCTCTGGGTCTTGGAGGGATGTGGGAAT
 CTCCTCGAACGGGAAGACCCAGGACCAAGGACTTCTCGAGTGGGTCTCTCCGAGTTTCGTCCGAAAAACGGGTCCGAGTCGAAACTAGATGTGGAGAACGGTGGAAAGAGTTCCTGACACTGGGAAACCCCTAAGCAGGGACTGGGACGAAGGGTTTCGAGAGGACCCAGAACTCCCTACACCCTTA

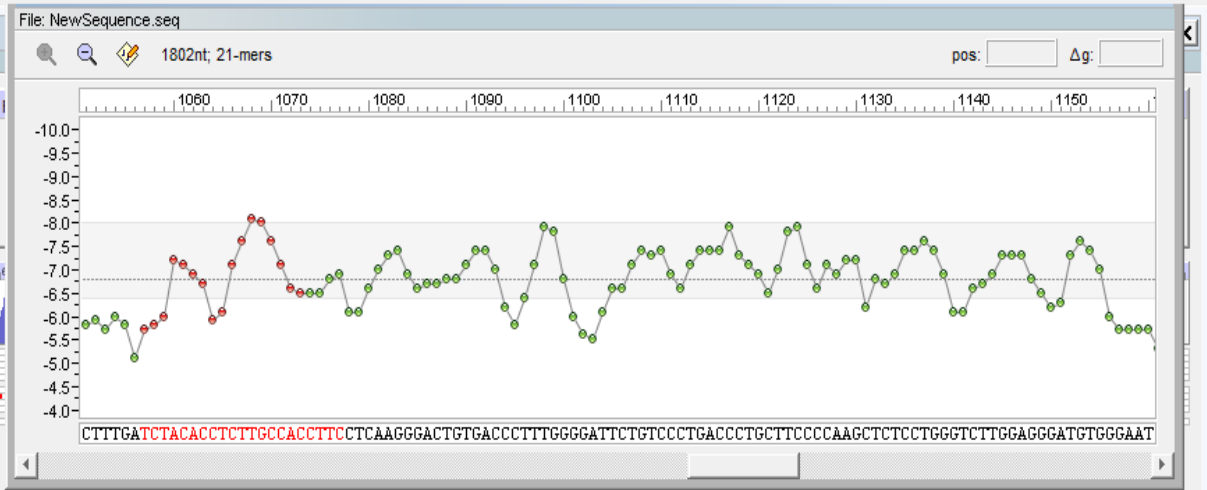
AGATGTGGAGAACGGTGGAAAGGAG

G A C P S G V L V P E E L T Q R G S K Q P F V P A Q L - S T P L A T F L K G L - P F G D S V P D P A S P S S P G S W R D V G M



Sequence
File: NewSequence.seq

DNA Sequence	Selected Oligo	Position	Length	#
Sequence Length: 1802 nt	<input checked="" type="checkbox"/> Forward Primer	736	21	
Reading Frame: +1	<input checked="" type="checkbox"/> Reverse Primer	1057	21	
Current Oligo Length: 21 nt	<input type="checkbox"/> Upper Oligo	---	---	
Position: 1057	<input type="checkbox"/> Lower Oligo	---	---	
t_m : 58.6°C	<input checked="" type="checkbox"/> PCR Product	[342,---] nt		



pos: tm:

980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150

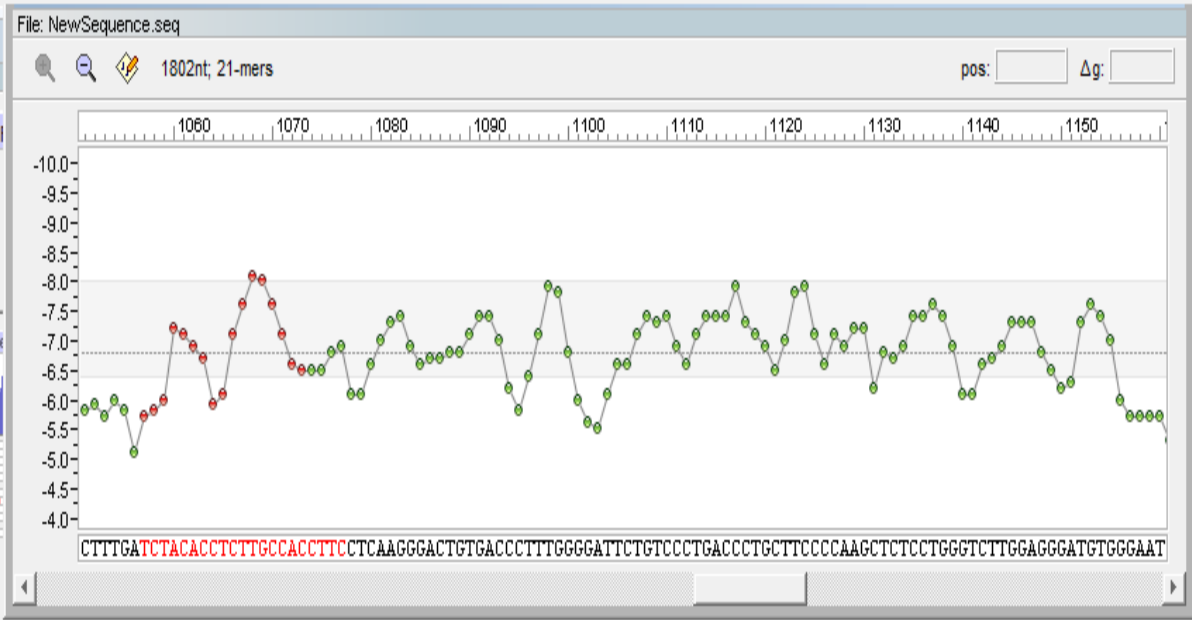
GAGGAGCTTGGCCCTTCTGGGGTCTGGTTCCTGAAGAGCTCACCCAGAGAGGCTCAAAGCAGCCCTTTTGTCCAGCTCAGCTTTGATCTACACCTCTTGCCACCTTCCTCAAGGGACTGTGACCCCTTTGGGGATTCTGTCCCTGACCCCTGCTTCCCAAGCTCTCTGGGTCTTGAGGGATGTGGGAAT
 CTCTCGAAGCGGAAGACCCAGGACCAAGGACTTCTCGAGTGGTCTCTCCGAGTTTCGTCGAAAAACAGGGTCGAGTCGAAACTAGATGTGGAGAACGGTGGAAAGAGTTCCTCGACACTGGGAAACCCCTAAGACAGGGACTGGGACCAAGGGGTTTCGAGAGGACCCAGAACCTCCCTACACCCCTTA

AGATGTGGAGAACGGTGGAAAG

G A C P S G V L V P E E L T Q R G S K Q P F V P A Q L - S T P L A T F L K G L - P F G D S V P D P A S P S S P G S W R D V G M

- Key Info
- Duplex Formation**
 - Forward Primer
 - Reverse Primer**
 - Upper Oligo
 - Lower Oligo
 - Current Oligo
 - Mixed Oligos
- Hairpin Formation
- Composition & Tm
- False Priming Sites
- Homology
- Selected Oligonucleotides
- Oligonucleotide Sets
- PCR
- LCR
- Melting Temperature Graph
- Internal Stability
- Sequence Frequency
- Open Reading Frames
- Restriction Enzyme Sites
- Restriction Enzyme Sites in Protein
- Hybridization Time
- Concentrations

All Checked Ctrl+X



pos: tm:

980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150

GAGGAGCTTGGCCCTTCTGGGGTCTGGTTCCTGAAGAGCTCACCCAGAGAGGCTCAAAGCAGCCCTTTGTCCAGCTCAGCTTTGATCTACACCTCTGCCACCTTCTCAAGGGACTGTGACCCCTTTGGGGATTCTGTCCCTGACCCTGCTTCCCCAAGCTCTCCTGGGTCTTGGAGGGATGTGGGAAT

CTCCTCGAACGGGAAGACCCAGGACCAAGGACTTCTCGAGTGGGTCTCTCCGAGTTTCTCGGAAAAACAGGGTCGAGTCGAAACTAGATGTGGAGAACGGTGGAAAGGAGTTCCTTGACACTGGGAAACCCCTAAGACAGGGACTGGGACGAAGGGGTTTCGAGAGGACCCAGAACCCTCCCTACACCTTA

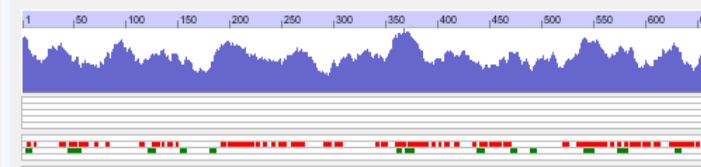
AGATGTGGAGAACGGTGGAAAGGAG

G A C P S G V L V P E E L T Q R G S K Q P F V P A Q L - S T P L A T F L K G L - P F G D S V P D P A S P S S P G S W R D V G M



Sequence
File: NewSequence.seq

DNA Sequence	Selected Oligo	Position	Length	#	F
Sequence Length: 1802 nt	<input checked="" type="checkbox"/> Forward Primer	736	21		
Reading Frame: +1	<input checked="" type="checkbox"/> Reverse Primer	1057	21		
Current Oligo Length: 21 nt	<input type="checkbox"/> Upper Oligo	---	---		
Position: 1057	<input type="checkbox"/> Lower Oligo	---	---		
t_m : 58.6°C	<input checked="" type="checkbox"/> PCR Product	[342,---] nt			



File: NewSequence.seq
Reverse Primer NewSequence:1057R21

Free 3'-end

The most stable dimer overall: # of hydrogen bonds = 4, $\Delta G = -3.8$ kcal/mol

5' GAAGGTGGCAAGAGGTGTAGA 3'

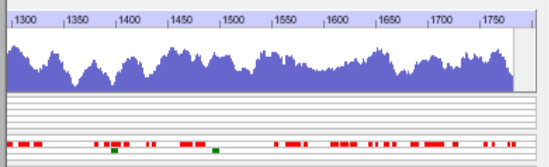
3' AGATGTGGAGAACGGTGGAAAG 5'

Hairpin loop: no stems found.

Handwritten red annotations:
- A red circle around $\Delta G = -3.8$ kcal/mol with a checkmark.
- Red arrows pointing to the sequence alignment.

File: NewSequence.seq

DNA Sequence	Selected Oligo	Position	Length	#	F
Sequence Length: 1802 nt	<input checked="" type="checkbox"/> Forward Primer	736	21		
Reading Frame: +1	<input checked="" type="checkbox"/> Reverse Primer	1057	21		
Current Oligo Length: 21 nt	<input type="checkbox"/> Upper Oligo	---	---		
Position: 1057	<input type="checkbox"/> Lower Oligo	---	---		
t_m : 58.6°C	<input checked="" type="checkbox"/> PCR Product	[342,---] nt			



pos: tm:

980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150

GAGGAGCTTGCCTTCTGGGGTCTGGTTCCTGAAGAGCTCACCCAGAGAGGCTCAAAGCAGCCTTTTGTCCAGCTCAGCTTTGATCTACACCTCTTGCACCTTCTCAAGGGACTGTGACCCTTTGGGATTCTGTCCCTGACCCTGCTTCCCCAAGCTCTCCTGGTCTTGGAGGGATGTGGGAATCTCTCGAACGGGAAGACCCAGGACCAAGACTTCTCGAGTGGTCTCTCCGAGTTTCGTGGAAAACAGGGTCGAGTCCGAAACTAGATGTGGAGAACGGTGGAAAGAGTTCCCTGACACTGGGAAACCCCTAAGACAGGGACTGGACGAAGGGGTTCCAGAGGACCCAGAACCTCCTACACCTTA

AGATGTGGAGAACGGTGGAAAG

G A C P S G V L V P E E L T Q R G S K Q P F V P A Q L - S T P L A T F L K G L - P F G D S V P D P A S P S S P G S W R D V G M

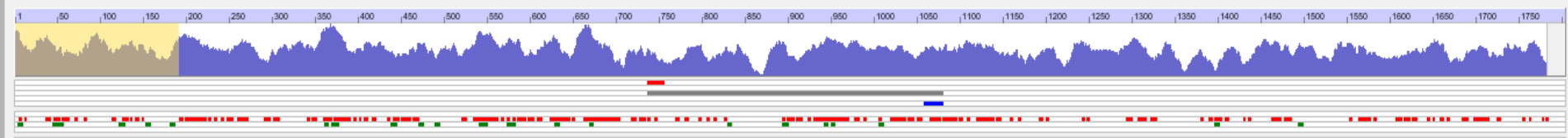


File: NewSequence.seq

DNA Sequence
Sequence Length: 1802 nt
Reading Frame: +1
Current Oligo Length: 21 nt
Position: 1
tm: 70.6°C

Selected Oligo	Position	Length
Forward Primer	736	21
Reverse Primer	1057	24
Upper Oligo	---	---
Lower Oligo	---	---
PCR Product	[345,---] nt	

#	Feature	Location
---	---------	----------



pos: tm:

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AGACCCCGGGCACCCGAGCAGGATCAAGGGAGGTGACGACGGGGACGCTCTCCGGAGTACGTGTCTACTGGTAACGACAACCAAGTTTCTCTCCGCGCTTTCCCGACCCGAGACCAGAGATCTCACGAGGTGGACACGAAGAGTGGCCATGGAAACCGCTACAAACCTCCGTAATGATCAACA
S G A R G V V L - F P P L L P L Q K A S C T D D H C C W F K G G G K G A G L W S L E C S S L C F S P G T F G D V W R H Y - L S

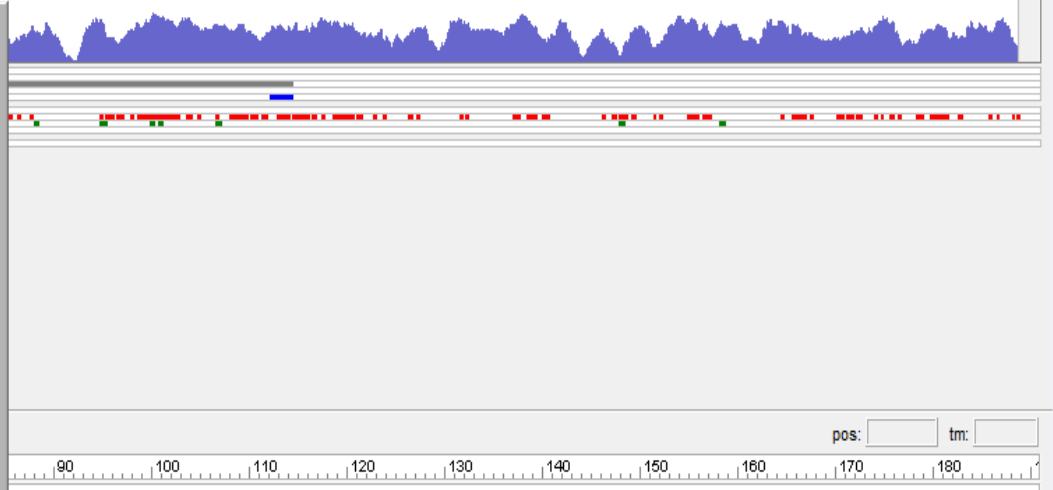


DNA Sequence	Selected Oligo	Position	Length	#	Feature	Location
Sequence Length: 1802 nt	<input checked="" type="checkbox"/> Forward Primer	736	21			
Reading Frame: +1	<input checked="" type="checkbox"/> Reverse Primer	1057	24			
Current Oligo Length: 21 nt	<input type="checkbox"/> Upper Oligo	---	---			
Position: 1	<input type="checkbox"/> Lower Oligo	---	---			
T_m : 70.6°C	<input checked="" type="checkbox"/> PCR Product	[345,---] nt				

Selected Primers

File: NewSequence.seq

NewSequence:736F21		NewSequence:1057R24	
5' ATGGGAAGACCCAGTTAGCGT 3'		5' GAGGAAGGTGGCAAGAGGTGTAGA 3'	
Length:	21-mer	Length:	24-mer
Score:	729 points	Score:	781 points
5' Position:	736	3' Position:	1057
T_m :	60.6 °C	T_m :	62.8 °C
$\Delta G/\Delta g$ (25 °C):	-32.0 kcal/mol	$\Delta G/\Delta g$ (25 °C):	-36.6 kcal/mol
$\Delta S/\Delta s$:	-429.1 cal/K * mol	$\Delta S/\Delta s$:	-497.5 cal/K * mol
$\Delta H/\Delta h$:	-160.0 kcal/mol	$\Delta H/\Delta h$:	-184.9 kcal/mol
3' ΔG :	-8.3 kcal/mol	3' ΔG :	-5.7 kcal/mol
Degeneracy:	1	Degeneracy:	1
P.E.#:	494/494	P.E.#:	500/500
1.E:	4.72 nmol/A ₂₆₀	1.E:	3.86 nmol/A ₂₆₀
	31.0 µg/A ₂₆₀		29.6 µg/A ₂₆₀



TCTGGGGCCCGTGGCGTCTCTCTAGTTCCTCCACTGCTGCCCTCGAGAAGGCCTCATGCACAGATGACCATTTGCTGTTGGTTCAAAGGAGGAGGCGGGAAAGGGGCTGGGCTCTGGTCTCTAGAGTGTCTCCAGCCTGTGCTTCTCACCCGGTACCTTTGGCGATGTTTGAGGCATTACTAGTGT
 AGACCCCGGGCACCAGCAGGAGATCAAGGGAGGTGACGACGGGGACGCTCTCCGGAGTACGTGTCTACTGGTAACGACAACCAAGTTTCTCTCCGCCCTTTCCCGACCCGAGACAGAGATCTCACGAGGTGGGACACGAAGAGTGGGCCATGGAAACCGCTACAAACCTCCGTAATGATCAACA

S G A R G V V L - F P P L L P L Q K A S C T D D H C C W F K G G G G K G A G L W S L E C S S L C F S P G T F G D V W R H Y - L S







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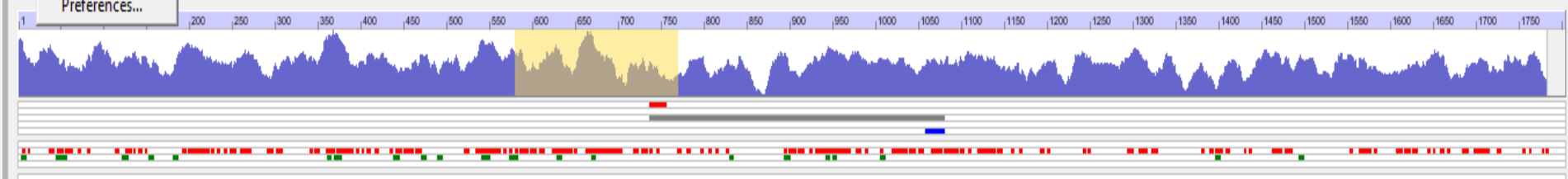
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- Primer-BLAST**
Design primers specific to your PCR template
- Global Align**
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- CD-search**
Find conserved domains in your sequence
- IgBLAST**
Search immunoglobulins and T cell receptor sequences
- VecScreen**
Search sequences for vector contamination
- CDART**
Find sequences with similar conserved domain architecture
- Multiple Alignment**
Align sequences using domain and protein constraints

- Entire Sequence
- Forward Primer
- Reverse Primer
- Upper Oligo
- Lower Oligo
- Restore
- Features
- Preferences...

	Selected Oligo	Position	Length
1802 nt	Forward Primer	736	21
+1	Reverse Primer	1057	24
21 nt	Upper Oligo	---	---
749	Lower Oligo	---	---
52.9°C	PCR Product	[345,---] nt	

#	Feature	Location



pos: tm:

580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760

ATGGGAAGACCCAGTTAGCGT

AGGAATGGCCCCAGCCTTGCACTGGAGTAGAGTCCTTGGCATTACAGCAGCTGGCCTCGTGTGCCATCCATTAAGTGC AAGATGGCTGGGCCCCGGCCTCCTGCACAATGTGCCAGAGTCCGTCATTTATATCTCCTCCTGTAGCGGATATGGGAAGACCCAGTTAGCGTTGATCTCTCATTT
 TCCTTACCGGGGTCGGAACCTGTGACCTCATCTCAGGAACCGTAAGTGTGCTGACCGGAGCACACGGTAGGTAAITCACGTTCTACCGACCCGGGGGCGGAGGGACGTGTTACACGGGTCTCACGCAGTAAATATAGAGGAGGAACATCCGCCTATACCTTCTGGGTCAATCGCAACTAGAGAGTAAA

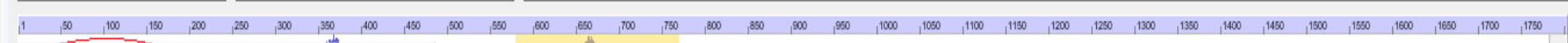
R N G P S L D T G V E S L A F T A A G L V C H P L S A R W L G P R P P C T M C P E C V I Y I S S L - A D M G R P S - R - S L I S



Sequence
File: NewSequence.seq

DNA Sequence	Selected Oligo	Position	Length
Sequence Length: 1802 nt	<input checked="" type="checkbox"/> Forward Primer	736	21
Reading Frame: +1	<input checked="" type="checkbox"/> Reverse Primer	1057	24
Current Oligo Length: 21 nt	<input type="checkbox"/> Upper Oligo	---	---
Position: 749	<input type="checkbox"/> Lower Oligo	---	---
t_m : 52.9°C	<input checked="" type="checkbox"/> PCR Product	[345,...] nt	

#	Feature	Location



Edit Forward Primer

File: NewSequence.seq

Accept/Discard Edit Search Change Rev.Translate

5'

Sequence Length: 21 nt	t_m : 60.6 °C
Reading Frame: 1	ΔG : -32.0 kcal/mol
Degeneracy: 1	Loop T_m : 51.8 °C
	Loop Δg : -1.6 kcal/mol

RT. Method: Lathe

Codons for ?

ctwt+c

1 10 20 30

ATG GGA AGA CCC AGT TAG CGT

M G R P S - R

5' ATGGGAA
3' TGCGATTGCCAG

Clipboard [21]: ATGGGAAGACCCAGTTAGCGT INS DNA

330 640 650 660 670 680 690 700 710 720 730 740 750 760

pos: t_m :

ATGGGAAGACCCAGTTAGCGT

GCTGGCCTCGTGTGCCATCCATTAAGTGC AAGATGGCTGGGCCCCCGCCCTCCCTGCACAATGTGCCAGAGTGGCTATTTATATCTCCTCCTGTAGGGGATATGGGAAGACCCAGTTAGCGTTGATCTCTCATTT
CGACCCGAGCACACGGTAGGTAATTCACGTTCTACCGACCCGGGGCGGGAGGGACGTGTACACGGGTCTCACGCAGTAAATATAGAGGAGGAACATCCGCCTATACCCCTCTGGGTCAATCGCAACTAGAGAGTAAA

A G L V C H P L S A R W L G P R P P C T M C P E C V I Y I S S L - A D M G R P S - R - S L I S

Primer-BLAST

A tool for finding specific primers

Finding primers specific to your PCR template (using Primer3 and BLAST).

Primers for target on one template

Primers common for a group of sequences

[Retrieve recent results](#) [Publication](#) [Tips for finding specific primers](#)

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PCR Template

Enter accession, gi, or FASTA sequence (A refseq record is preferred) [?](#) [Clear](#)

Or, upload FASTA file

[فایلی انتخاب نشده است](#) [انتخاب فایل](#)

Range [?](#) [Clear](#)

From To

Forward primer

Reverse primer

Primer Parameters

Use my own forward primer (5'->3' on plus strand)

[?](#) [Clear](#)

Use my own reverse primer (5'->3' on minus strand)

[?](#) [Clear](#)

PCR product size

Min Max

of primers to return

Primer melting temperatures (T_m)

Min Opt Max Max T_m difference [?](#)

Exon/intron selection

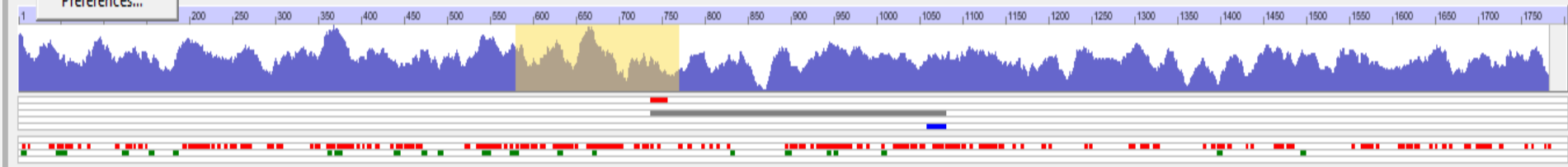
A refseq mRNA sequence as PCR template input is required for options in the section [?](#)

Even junctions only

- Entire Sequence
- Forward Primer
- Reverse Primer
- Upper Oligo
- Lower Oligo
- Restore
- Features
- Preferences...

	Selected Oligo	Position	Length
1802 nt	Forward Primer	736	21
+1	Reverse Primer	1057	24
21 nt	Upper Oligo	---	---
749	Lower Oligo	---	---
52.9°C	PCR Product	[345,---] nt	

#	Feature	Location



pos: tm:

580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760

ATGGGAAGACCCAGTTAGCGT

AGGAATGGCCCAGCCTTGACACTGGAGTAGAGTCCTTGGCATTACAGCAGCTGGCCTCGTGTGCCATCCATTAAGTGCAAGATGGCTGGGCCCCCGCCTCCCTGCACAATGTGCCAGAGTCCGTCATTTATATCTCCTCCTGTAGCGGATATGGGAAGACCCAGTTAGCGTTGATCTCTCATT
 TCCTTACCGGGGTCGGAACCTGTGACCTCATCTCAGGAACCGTAAGTGTGTCGACCGGAGCACACGGTAGGTAATTCACGTTCTACCGACCCGGGGGCGGGAGGACGTGTTACACGGGTCTCACGCAGTAAATATAGAGGAGGAACATCCGCCTATACCTTCTGGGTCAATCGCAACTAGAGAGTAAA

R N G P S L D T G V E S L A F T A A G L V C H P L S A R W L G P R P P C T M C P E C V I Y I S S L - A D M G R P S - R - S L I S



DNA Sequence	Selected Oligo	Position	Length	#	Feature	Location
				1		
				4		

Edit Reverse Primer

File: NewSequence.seq

Accept/Discard Edit Search Change Rev.Translate

3' 1057

Sequence Length: 24 nt t_m : 62.8 °C
 Reading Frame: 1 ΔG : -36.6 kcal/mol
 Degeneracy: 1 Loop T_m : ---- °C
 Loop Δg : ---- kcal/mol

RT. Method: Lathe

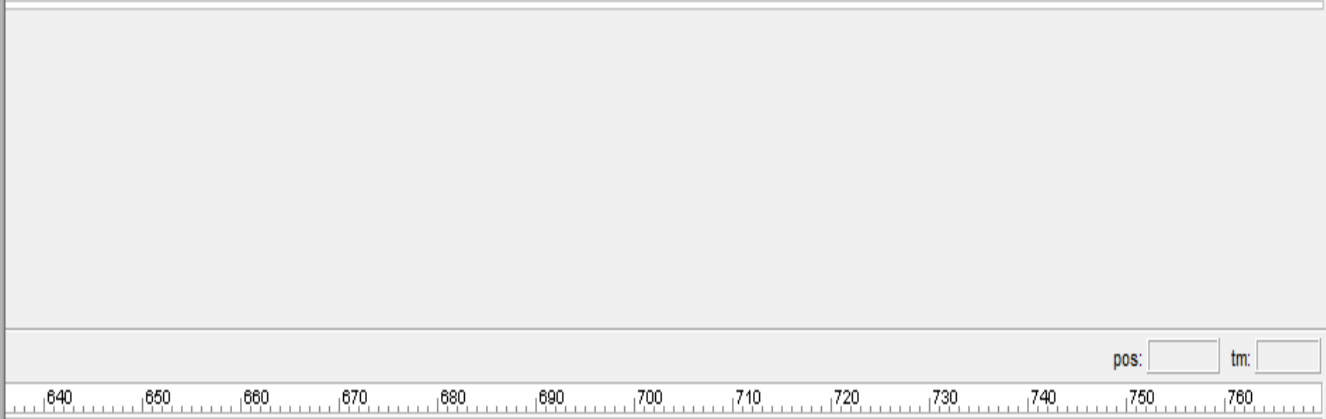
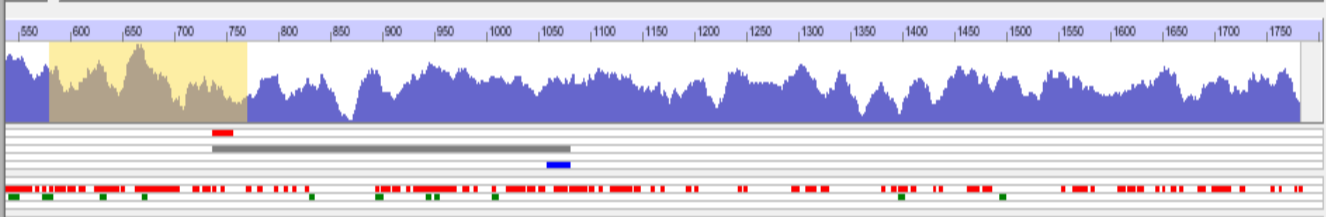
Codons for ?

1 10 20 30

GAG GAA GGT GGC AAG AGG TGT AGA

E E G G K R C R

No stems found.



Clipboard [24]: GAGGAAGGTGGCAAGAGGTGTAGA INS | DNA

ATGGGAAGACCCAGTTAGCGT

AGGAATGGCCCCAGCCTTGACACTGGAGTAGAGTCCCTTGGCATTACAGCAGCTGGCCTCGTGTGCCATCCATTAAGTGCAAGATGGCTGGGCCCCCGCCCTCCCTGCACAATGTGCCAGAGTCCGTCATTTATATCTCTCTCTGTAGGCGGATATGGGAAGACCCAGTTAGCGTTGATCTCTCATTTTCCTTACCGGGGTCGGAACCTGTGACCTCATCTCAGGAACCGTAAGTGTGCTCGACCGGAGCAGACACGGTAGGTAATTCACGTTCTACCGACCCGGGGCGGGAGGGACGTGTTACACGGGTCTCACGCAGTAAATATAGAGGAGGAACATCCGCTATACCTTCTGGGTC

R N G P S L D T G V E S L A F T A A G L V C H P L S A R W L G P R P P C T M C P E C V I Y I S S L - A D M G R P S - R - S L I S

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Primers for target on one template

Primers common for a group of sequences

[Retrieve recent results](#) [Publication](#) [Tips for finding specific primers](#)

[Save search parameters](#) [Reset page](#)

PCR Template

Enter accession, g

Or, upload FASTA

Primer Param

Use my own forwa

(5' -> 3' on plus stra

Use my own rever

>3' on minus strand)

PCR product size

of primers to return

Primer melting temperatures (T_m)

- Ctrl+Z وانگرد
- Ctrl+تبدیل+Z انجام مجدد
- Ctrl+X برش
- Ctrl+C کپی
- Ctrl+V جای‌گذاری
- Ctrl+تبدیل+V جای‌گذاری به عنوان متن ساده
- Ctrl+A انتخاب همه
- ← شل‌کنگر املا
- ← جهت نوشتن
- بازرس

referred) ? Clear

Range ? Clear

From To

Forward primer

Reverse primer

فایلی

TAGCGT ? Clear

? Clear

Min Max
70 1000

10

Min Opt Max Max T_m difference
57.0 60.0 63.0 3 ?

Exon/intron selection

A refseq mRNA sequence as PCR template input is required for options in the section ?

برای دریافت به روز رسانی‌های آبی Google Chrome، باید Windows 10 یا بالاتر داشته باشید. این رایانه از Windows 7 استفاده می‌کند.

Or, upload FASTA file

فایلی انتخاب نشده است انتخاب فایل

Forward primer From To
Reverse primer

Primer Parameters

Use my own forward primer (5'->3' on plus strand) ? Clear

Use my own reverse primer (5'->3' on minus strand) ? Clear

PCR product size
Min Max

of primers to return

Primer melting temperatures (T_m)
Min Opt Max Max T_m difference ?

Exon/intron selection

A refseq mRNA sequence as PCR template input is required for options in the section ?

Exon junction span ?

Exon junction match
Min 5' match Min 3' match Max 3' match
Minimal and maximal number of bases that must anneal to exons at the 5' or 3' side of the junction ?

Intron inclusion
Primer pair must be separated by at least one intron on the corresponding genomic DNA ?

Intron length range
Min Max ?

Note: Parameter values that differ from the default are highlighted in yellow

Intron length range
Min: 1000 Max: 10000

Note: Parameter values that differ from the default are highlighted in yellow

Primer Pair Specificity Checking Parameters

Specificity check: Enable search for primer pairs specific to the intended PCR template

Search mode: Automatic

Database: Refseq mRNA (highlighted), Refseq representative genomes (highlighted), Genomes for selected organisms (primary reference assembly only), nr, Refseq RNA (refseq_rna), Custom

Exclusion: Exclude uncultured/environmental sample sequences

Organism: organism (highlighted)

Entrez query (optional):

Primer specificity stringency: Primer must have at least 2 total mismatches to unintended targets, including at least 2 mismatches within the last 5 bps at the 3' end. Ignore targets that have 6 or more mismatches to the primer.

Max target amplicon size: 4000

Allow splice variants: Allow primer to amplify mRNA splice variants (requires refseq mRNA sequence as PCR template input)

Get Primers

Show results in a new window Use new graphic view

Note: Parameter values that differ from the default are highlighted in yellow

+ Advanced parameters

Intron length range	Min	Max
	<input type="text" value="1000"/>	<input type="text" value="10000"/>

Note: Parameter values that differ from the default are highlighted in yellow

Primer Pair Specificity Checking Parameters

Specificity check	Enable search for primer pairs specific to the intended PCR template ?	
Search mode	<input type="text" value="Automatic"/> ?	
Database	<input type="text" value="Refseq mRNA"/> ?	
Exclusion	Exclude predicted Refseq transcripts (accession with XM, XR prefix) Exclude uncultured/environmental sample sequences ?	
Organism	<input type="text" value="Homo sapiens"/> <input type="button" value="Add organism"/>	
	Enter an organism name (or organism group name such as enterobacteriaceae, rodents), taxonomy id or select from the suggestion list as you type. ?	
Entrez query (optional)	<input type="text"/>	
Primer specificity stringency	Primer must have at least <input type="text" value="2"/> total mismatches to unintended targets, including at least <input type="text" value="2"/> mismatches within the last <input type="text" value="5"/> bps at the 3' end. ? Ignore targets that have <input type="text" value="6"/> or more mismatches to the primer. ?	
Max target amplicon size	<input type="text" value="4000"/> ?	
Allow splice variants	Allow primer to amplify mRNA splice variants (requires refseq mRNA sequence as PCR template input) ?	

?

Note: Parameter values that differ from the default are highlighted in yellow

+ Advanced parameters

An official website of the United States government. Here's how you know.

Log in

Primer-BLAST

A tool for finding specific primers

Making primers specific to your PCR template. [more...](#)

Status	Submitted	Check
Current time	27 February 2023, 14:59:20	

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Primer-BLAST

Primer-BLAST Results

Input PCR template none

Specificity of primers Target templates were found in selected database: RefSeq Representative Genome Database (Organism limited to Homo sapiens)

Other reports [Search Summary](#)

Detailed primer reports

Primer pair 1

	Sequence (5'→3')	Length	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	ATGGGAAGACCCAGTTAGCGT	21	61.18	52.38	4.00	0.00
Reverse primer	GAGGAAGGTGGCAAGAGGTGTAGA	24	63.66	54.17	3.00	2.00

Products on target templates

>NC_000012.12 Homo sapiens chromosome 12, GRCh38.p14 Primary Assembly

product length = 345

Features associated with this product:

- [corrinoid adenosyltransferase precursor](#)
- [corrinoid adenosyltransferase isoform x3](#)

Forward primer 1 ATGGGAAGACCCAGTTAGCGT 21
 Template 109557209 109557189

Detailed primer reports

Primer pair 1

	Sequence (5'→3')	Length	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	ATGGGAAGACCCAGTTAGCGT	21	61.18	52.38	4.00	0.00
Reverse primer	GAGGAAGGTGGCAAGAGGTGTAGA	24	63.66	54.17	3.00	2.00

Products on target templates

>NC_000012.12 Homo sapiens chromosome 12, GRCh38.p14 Primary Assembly

product length = 345

Features associated with this product:

[corrinoid adenosyltransferase precursor](#)

[corrinoid adenosyltransferase isoform x3](#)

```

Forward primer 1      ATGGGAAGACCCAGTTAGCGT  21
Template          109557209 ..... 109557189

Reverse primer 1      GAGGAAGGTGGCAAGAGGTGTAGA  24
Template          109556865 ..... 109556888

```