

Primer design



Gene

Gene

BiP AND Homo sapiens

Search

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Genomic

Categories

Alternatively spliced
Annotated genes
Protein-coding

Sequence content

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See [HSPA5 \(BiP\) heat shock protein family A \(Hsp70\) member 5](#) in the Gene database
bip in [Homo sapiens \(2\)](#) [All 2 Gene records](#)Filters: [Manage Filters](#)

Search results

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Results by taxon

Top Organisms [Tree](#)Homo sapiens (76)
Candida albicans SC5314 (1)
Human immunodeficiency virus 1 (1)

Find related data

Database: Select

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Search details

BiP[All Fields] AND ("Homo sapiens"
[Organism] OR Homo sapiens[All Fields])
AND alive[prop]

Search

See more...

clear

Name/Gene ID	Description	Location	Aliases	MIM
<input type="checkbox"/> HSPA5 ID: 3305	heat shock protein family A (Hsp70) member 5 [<i>Homo sapiens</i> (human)]	Chromosome 9, NC_000009.12 (125234848..125241387, complement)	BiP , GRP78, HEL-S-89n, MIF2	138120
<input type="checkbox"/> GDF10 ID: 2662	HSPA5: a synonymous name of BiP (human)]		BIP, BMP-3b, BMP3B	601361
<input type="checkbox"/> SIL1 ID: 64374	SIL1 nucleotide exchange factor [<i>Homo sapiens</i> (human)]	Chromosome 5, NC_000005.10 (138946720..139198376, complement)	BAP, MSS, ULG5	608005
<input type="checkbox"/> HLA-B ID: 3106	major histocompatibility complex, class I, B [<i>Homo sapiens</i> (human)]	Chromosome 6, NC_000006.12 (31353866..31357245, complement)	AS, B-4901, HLAB	142830
<input type="checkbox"/> MAPT	microtubule associated	Chromosome 17, NC_000017.11	DDPAC, FTDP-17L,	157140

**Genomic**1. **NG_027761.1 RefSeqGene**

Range	5001..11540
Download	GenBank , FASTA , Sequence Viewer (Graphics)

mRNA and Protein(s)1. **NM_005347.4 → NP_005338.1 endoplasmic reticulum chaperone BiP precursor**[See identical proteins and their annotated locations for NP_005338.1](#)**Status: REVIEWED**

Source sequence(s)	AA433933 , BC020235 , DA549454 , X87949
Consensus (COS)	CCDS6863.1
UniProtKB/Swiss-Prot	P11021
UniProtKB/TrEMBL	V9HWB4
Related	ENSP00000324173.6 , OTTHUMP00000022124 , ENST00000324460.6 , OTTHUMT00000054062

Conserved Domains (1) [summary](#)

pfam00012	HSP70; Hsp70 protein
Location:30 → 635	

☒ [RefSeqs of Annotated Genomes: Homo sapiens Annotation Release 109 details...](#)

The following sections contain reference sequences that belong to a specific genome build. [Explain](#)

Reference GRCh38.p12 Primary Assembly**Genomic**

**Nucleotide Sequence (1965 nt):**

```

ATGAAGCTCTCCCTGGTGGCCGCGATGCTGCTGCTGCTCAGCGCGGGCGGGCCGAGGAGGAGGACAAGA
AGGAGGACGTGGGCACGGTGGTCGGCATCGACCTGGGGACCACCTACTCCTGCGTCGGCGTGTTCAGAA
CGGCCGCGTGGAGATCATCGCAACGATCAGGGCAACCGCATCACGCCGTCCTATGTCGCCTTCACTCCT
GAAGGGGAACGTCTGATTGGCGATGCCGCAAGAACCAGCTCACCTCCAACCCCGAGAACACGGTCTTTG
ACGCCAAGCGGCTCATCGGCCGACGTTGGAATGACCCGCTCTGTGCAGCAGGACATCAAGTTCTTGCCGTT
CAAGGTGGTTGAAAAGAAAATAAACCATACATTCAAGTTGATATTGGAGGTGGGCAACAAAGACATTT
GCTCCTGAAGAAATTTCTGCCATGGTCTCACTAAAATGAAAGAAACCGCTGAGGCTTATTTGGGAAAGA
AGGTTACCCATGCAGTTGTTACTGTACCAGCCTATTTAATGATGCCCAACGCCAAGCAACCAAGACGC
TGGAACTATTGCTGGCCTAAATGTTATGAGGATCATCAACGAGCCTACGGCAGCTGCTATTGCTTATGGC
CTGGATAAGAGGGAGGGGAGAAGAACATCCTGGTGTGGTGGCTGGGCGGAACCTTCGATGTGTCTC
TTCTCACCAITGACAATGGTGTCTTCGAAGTTGGGCCACTAATGGAGATACTCATCTGGGTGGAGAAGA
CTTTGACCAGCGTGTGATGGAACACTTCATCAAACCTGTACAAAAAGAAGACGGGCAAGATGTCAGGAAA
GACAAATAGAGCTGTGCAGAAACTCCGGCGCAGGTAGAAAAGGCCAAACGGGCCCTGTCTTCTCAGCATC
AAGCAAGAATTGAAATTGAGTCTTCTATGAAGGAGAAGACTTTTCTGAGACCCTGACTCGGGCCAAATT
TGAAGAGCTCAACATGATCTGTTCCGGTCTACTATGAAGCCCGTCCAGAAAGTGTGGAAAGATTCTGAT
TTGAAGAAGTCTGATATTGATGAAATTTGTTCTTGTGGTGGCTCGACTCGAATCCAAAGATTGAGCAAC
TGGTTAAAGAGTTCTTCAATGGCAAGGAACCATCCCGTGGCATAAACCCAGATGAAGCTGTAGCGTATGG
TGCTGCTGTCCAGGCTGGTGTGCTCTCTGGTGTCAAGATACAGGTGACCTGGTACTGCTTGATGTATGT
CCCCTTACACTTGGTATTGAAACTGTGGGAGGTGTCATGACCAAACTGATCCAAAGAACACAGTGGTGC
CTACCAAGAAGTCTCAGATCTTTTCTACAGCTTCTGATAATCAACCAACTGTTACAATCAAGGTCTATGA
AGGTGAAAGACCCCTGACAAAAGACAATCATCTTCTGGGTACATTTGATCTGACTGGAATTCTCCTGCT
CCTCGTGGGGTCCCACAGATTGAAGTACCTTTGAGATAGATGTGAATGGTATTCTTCGAGTGACAGCTG
AAGACAAGGGTACAGGGAAACAAAATAAGATCACCAATCACCAATGACCAGAATCGCCTGACACCTGAAGA
AATCGAAAGGATGGTTAATGATGCTGAGAAGTTTCTGAGGAAGACAAAAGCTCAAGGAGCGCATTGAT
ACTAGAAATGAGTTGGAAAAGCTATGCCTATTCTCTAAAGAATCAGATTGGAGATAAAGAAAAGCTGGGAG
GTAAACTTTCTCTGAAGATAAGGAGACCATGGAAAAGCTGTAGAAGAAAAGATTGAATGGCTGGAAAAG
CCACCAAGATGCTGACATTGAAGACTTCAAAGCTAAGAAGAAGGAAGCTGGAAGAAATTTGTTCAACCAATT
ATCAGCAAACTCTATGGAAGTGCAGGCCCTCCCCAACTGGTGAAGAGGATACAGCAGAAAAGATGAGT
TGTAG

```

copy

Translation (654 aa):

```

MKLSLVAAML LLLS AARAE EEDKKE DVGTVV GIDL GTTYS CVGV FKNR VEI IAND QNRI TPSY VVAF TP
EGER LIGDAA KNQLT SNPENT VFDA KR LI GR TWND PSVQ QDI KFL PFKV VEKTK PYIQVD IGGG QIKT F
APEE ISAMV LTKMKETA EAYLGK KVTHAV VTVPAY FNDA QRQAT KDA GTIAG LNVMRI INE P TAAAIAYG
LDKRE GEKNIL VFDLGGT F DVSL TI DNGV FEVVAT NGDTHLGGED FDFQ RVM EHF I KLYKKKT GK D VRK
DNRAV QKLR REVEKAKRALSSQH QARIE IESFYEGED FSETL TRAKFEELNMDLFR STMKPVQKVLEDS D
LKKSDI DEIVLVGGSTRIPKIQQLVKEFFNGKEPSRGINPDEAVAYGAAVQAGVLSGDQDTGDLVLLDVC

```


paste

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

```
AATCGAAAAGGATGGTTAATGATGCTGAGAAAGTTTGGCTGAGGAAGACAAAAGCTCAAGGAGCCATTGAT
ACTAGAAAATGAGTTGGAAAAGCTATGCCATTTCTCTAAAAGAATCAGATGGAGATAAGAAAAAGCTGGGAG
GTAAACTTTCTCTGAAGATAAGGAGACCATGGAAAAAGCTGTAGAAGAAAAGATTGAATGGCTGGAAG
CCACCAAGATGCTGACATGAAGACTTCAAAGCTAAGAAGAAGGAAGCTGGAAGAAAATTTCAACCAATT
ATCAGCAAACCTCTATGGAAGTGCAGGCCCTCCCCCAACTGGTGAAGAGGATACAGCAGAAAAAGATGAGT
TGTAG
```

Or, upload FASTA file

参照... ファイルが選択されていません。

Range

Forward primer From To [Clear](#)
Reverse primer

<https://www.ncbi.nlm.nih.gov/tools/primer-blast/>

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

Search mode
Database
Exclusion Exclude predicted Refseq transcripts (accession with XM, XR prefix) Exclude uncultured/environmental sample sequences

Organism
Enter an organism name (or organism group name such as enterobacteriaceae, rodents), taxonmv id or select from the suggestion list as you type.

Choose species

Entrez query (optional)
Primer specificity stringency
Primer must have at least total mismatches to unintended targets, including
at least mismatches within the last bps at the 3' end.
Ignore targets that have or more mismatches to the primer.
Max target size
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

▶ NCBI/ Primer-BLAST: Finding primers specific to your PCR template (using Primer3 and BLAST).

Input PCR template

Range 1 - 1965

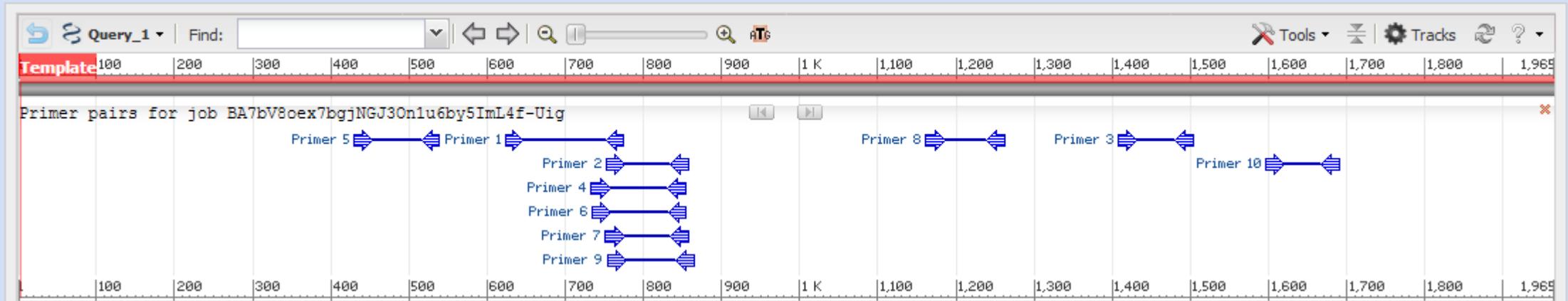
Your PCR template is highly similar to the following sequence(s) from the search database. To increase the chance of finding specific primers, please review the list below and select all sequences (within the given sequence ranges) that are intended or allowed targets.

Select: [All](#) [None](#) Selected:0

Accession	Title	Identity	Alignment length	Seq. start	Seq. stop
<input checked="" type="checkbox"/> NM_005347.4	Homo sapiens heat shock protein family A (Hsp70) member 5 (HSPA5), mRNA	100%	1965	262	2226

 Show results in a new window

Graphical view of primer pairs



Primer pair 1

	Sequence (5'->3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	TATGGCCTGGATAAGAGGGAG	Plus	21	625	645	58.09	52.38	4.00	0.00
Reverse primer	AAGTCTTCTCCACCCAGATGA	Minus	21	773	753	58.09	47.62	5.00	2.00
Product length	149								

Products on intended target

>[NM_005347.4](#) Homo sapiens heat shock protein family A (Hsp70) member 5 (HSPA5), mRNA

product length = 149

```

Forward primer 1  TATGGCCTGGATAAGAGGGAG  21
Template       886  .....  906

Reverse primer 1  AAGTCTTCTCCACCCAGATGA  21
Template       1034 .....  1014
    
```

Primer pair 2

	Sequence (5'->3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	TCATCTGGGTGGAGAAGACTTTG	Plus	23	753	775	59.99	47.83	5.00	1.00
Reverse primer	TGCACAGCTCTATTGTCTTTCCT	Minus	23	857	835	59.99	43.48	4.00	0.00
Product length	105								

product length = 107
 Forward primer 1 CTCATCTGGGTGGAGAAGACTTTG 24
 Template 1013 1036
 Reverse primer 1 CTGCACAGCTCTATTGTCTTTCT 24
 Template 1119 1096

Primer pair 8

	Sequence (5'->3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	ATAAACCAGATGAAGCTGTAGCG	Plus	24	1162	1185	60.98	45.83	4.00	2.00
Reverse primer	GGACATACATCAAGCAGTACCAGG	Minus	24	1262	1239	60.98	50.00	4.00	3.00
Product length	101								

Products on intended target

>[NM_005347.4](#) Homo sapiens heat shock protein family A (Hsp70) member 5 (HSPA5), mRNA

product length = 101
 Forward primer 1 ATAAACCAGATGAAGCTGTAGCG 24
 Template 1423 1446
 Reverse primer 1 GGACATACATCAAGCAGTACCAGG 24
 Template 1523 1500

Primer pair 9

	Sequence (5'->3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CATCTGGGTGGAGAAGACTTTGAC	Plus	24	754	777	61.10	50.00	5.00	1.00
Reverse primer	GGAGTTTCTGCACAGCTCTATTGT	Minus	24	865	842	61.10	45.83	4.00	0.00
Product length	112								

Products on intended target

>[NM_005347.4](#) Homo sapiens heat shock protein family A (Hsp70) member 5 (HSPA5), mRNA

product length = 112
 Forward primer 1 CATCTGGGTGGAGAAGACTTTGAC 24
 Template 1015 1038
 Reverse primer 1 GGAGTTTCTGCACAGCTCTATTGT 24
 Template 1126 1103



Human (GRCh38.p12) ▾

<http://asia.ensembl.org/index.html>

Search Human (*Homo sapiens*)

Search all categories ▾

HSPA5

Go

e.g. [BRCA2](#) or [17:63992802-64038237](#) or [rs1333049](#) or [osteoarthritis](#)

What's New in Human release 92

- Update to Ensembl-Havana human GENCODE gene set (release 28)
- Updated human otherfeatures db: New CCDS import
- HGMD Public dataset

Current selection:

< all Species

Only searching Human

Only searching Human ▾

HSPA5



2435 results match HSPA5 when restricted to

species: Human ✕

Restrict category to:

Gene	3
Transcript	1
Somatic Mutation	150
GeneTree	1
ProbeFeature	51
Protein Family	1
Variant	2228

Per page:

10 25 50 100

Layout:

[HSPA5 \(Human Gene\)](#)

[ENSG00000044574](#) 9:125234853-125241330:-1

Heat shock protein family A (Hsp70) member 5 [Source:HGNC Symbol;Acc:HGNC:5238]

HEAT-SHOCK 70-KD PROTEIN 5; *HSPA5* [*138120] (MIM gene record; description: HEAT-SHOCK 70-KD PROTEIN 5; *HSPA5*; GLUCOSE-REGULATED PROTEIN, 78-KD; GRP78; IMMUNOGLOBULIN HEAVY CHAIN-BINDING PROTEIN; BIP.) is an external reference matched to Gene ENSG00000044574

[Variant table](#) • [Phenotypes](#) • [Location](#) • [External Refs.](#) • [Regulation](#) • [Orthologues](#) • [Gene tree](#)

[HSPA5-201 \(Human Transcript\)](#)

[ENST00000324460](#) 9:125234853-125241330:-1

Heat shock protein family A (Hsp70) member 5 [Source:HGNC Symbol;Acc:HGNC:5238].

[Location](#) • [External Refs.](#) • [cDNA seq.](#) • [Exons](#) • [Variant table](#) • [Protein seq.](#) • [Population](#) • [Protein summary](#)

[HSPA5 \(Human Gene\)](#)

[3309](#) 9:125234848-125241387:-1

Hspa5.

[Variant table](#) • [Phenotypes](#) • [Location](#) • [External Refs.](#) • [Regulation](#) • [Orthologues](#) • [Gene tree](#)

[PTHR13388_SF6 \(Human Protein Family\)](#)

[PTHR13388_SF6](#)

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Genomic browser interface showing gene tracks for RABEPK-206, RABEPK-201, RABEPK-204, RABEPK-202, and HSPA5-201. A red dashed circle highlights the HSPA5-201 gene track, and a red arrow points to the 'Exons' link in the HGNC Symbol popup window.

Gene Legend

Protein Coding	Non-Protein Coding
■ Ensembl protein coding	■ processed trans
■ merged Ensembl/Havana	

Regulation Legend

■ Open Chromatin	■ Promoter
■ Promoter Flank	■ Motif feature

HGNC Symbol: HSPA5

Gene	heat shock protein family A (Hsp70) member 5
Location	Chromosome 9: 125,234,853-125,241,330
Transcript	HSPA5-201
Protein	ENSP00000324173
Gene type	Protein coding
Transcript type	Protein coding
Strand	Reverse
Base pairs	3,908
Amino acids	654

Configuring the display

Tip: use the "Configure this page" link on the left to show additional data in this region.

- Original probes
- Supporting evidence
- ID History
- Transcript history
- Protein history

- Configure this page
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Exons/ Introns [Translated sequence](#) [Flanking sequence](#) [Intron sequence](#) [UTR](#)

Variants [Downstream](#) [Frameshift](#) [Inframe deletion](#) [Inframe insertion](#) [Intronic](#) [Missense](#) [Splice donor](#) [Splice region](#)

[Stop gained](#) [Synonymous](#) [Upstream](#)

Markup loaded

Show **All** entries [Show/hide columns](#)

No.	Exon / Intron	Start	End	Start Phase	End Phase	Length	Sequence
	5' upstream sequence					gggaagggtatataaagccgagtagggcagcggtagggtcagcgcggccaag
1	ENSE00001460790	125,241,330	125,241,005	-	2	326	ACAGCACAGACAGATTGACCTATTGGGGTGTTCGCGAGTGTGAGAGGGGAAGCGCCGCGG CCTGTATTTCTAGACCTGCCCTTCGCCTGGTTCGTGGCGCCTTGTGACCCCGGGCCCTTG CCGCCTGCAAGTCGGAAATTGCGCTGTGCTCCTGTGCTACGGCCTGTGGCTGGACTGCCT GCTGCTGCCCACTGGCTGGCAAGATGAAGCTCTCCCTGGTGGCCCGGATGCTGCTGCTG CTCAGCGCGCGGGCCGAGGAGGAGGACAGAGAGGAGGACGTGGCACGGTGGTCGGC ATCGACTGGGGACCACCTACTCTCTG
	Intron 1-2	125,241,004	125,240,908			97	gtaagtggggttgcggatgcagggggacggggcgtggccgcctggcctggcgtgaagaagt gcggtgctgatgtccctctgtcggggtttttctgcag
2	ENSE00000983644	125,240,907	125,240,676	2	0	232	CGTCGGCGTGTTCAAGAACGGCCGCGTGGAGATCATCGCCAACGATCAGGGCAACCGCAT CACGCCGTCTATGTCGCCTTCACTCCTGAGGGGACGTCTGATTGGGATGCCGCCAA GAACCAGCTCACCTCAACCCCGAGAACACGGTCTTTGACGCCAAGCGGCTCATCGGCCG CAGGTGGAATGACCCGTTCTGTGCAGCAGGACATCAAGTTCTTGCCTTCAAG
	Intron 2-3	125,240,675	125,240,310			366	gttcaccgggtttttctcatccagtttagagaacgggtgggtggtgggagtatttagagt tataagtctctggaaaagtgttgagacaacagttgagggttatagacatgatgtatgtaa taactttaactatattagtagttacaaaacttaagacagttgctgtcgtactgtctacg atagtttaggaataaaagaccgattaaaactgaactttgtaagacacctaactccctga agtatttctagtcaatttgacgccccaaaggacaaaataaaccaattgtggggatggt agtgggtcttttaaaccttgagatgtcatctgtatctgtgtctgaaaacaataattcttta aaatag
3	ENSE00000983645	125,240,309	125,240,172	0	0	138	GTGGTTGAAAAGAAAATAAACCATACATTCAAGTTGATAATGGAGGTGGCCAAACAAAG ACATTTGCTCCTGAAGAAATTTCTGCCATGGTTCTCACTAAAATGAAAGAAACCGCTGAG GCTTATTTGGGAAAAGAAG

- Oligo probes
- Supporting evidence
- ID History
- Transcript history
- Protein history

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Exons/ Introns Translated sequence Flanking sequence Intron sequence UTR

Variants Downstream Frameshift Inframe deletion Inframe insertion Intronic Missense Splice donor Splice region

Stop gained Synonymous Upstream

Markup loaded

Show All entries Filter

Show/hide columns

- No.
- Exon / Intron
- Start
- End
- Start Phase
- End Phase
- Length
- Sequence

Length	Sequence
326	<p>.....</p> <p>ACAGCACA</p> <p>CCTGTATT</p> <p>CCGCCTGC</p> <p>GCTGCTGC</p> <p>CTCAG</p> <p>ATCGA</p>
97	<p>gtaagtgg</p> <p>gagggtgctgatgtccctdgtcgggtttttctgcag</p>
232	<p>CGTCGGGTGTTCAAGAACGGCCCGTGGAGATCATCGCAACGATCAGGGCAAACGCAT</p> <p>CAGCCGTCCTATGTCGCCTCACTCCGAAAGGGAAAGTCTGATGGGATGCCGCCAA</p> <p>GAACCAGCTCACCTCAACCCGAGAACACGGTCTTGACGCCAAGGGCTCATGGCCG</p> <p>CAGGTGAATGACCGTCTGTGCAGCAGGACATCAAGTTCTGCGTTCAAG</p>
366	<p>gttcgaccgggtttttctcatccagttagagaacgggtgggtggtgggagtatttagagt</p> <p>tataagtctctggaaaagtgtgagacaacagttgagggttatagacatgatgtatgtaa</p> <p>taactttaatactattagtagttacaaaacttaagacagttgctgtcgtactgtctacg</p> <p>atagtttaggaataaaagaccgattaaaactgaactttgtaagacacctatactccctga</p> <p>agtattctagtcaatttgcagcccaagggaccaaaataaaccaaattgtggggatggt</p> <p>agtgggtcttttaactttgagatgtcatctgtatctgtgtctgaaaacaataattcttta</p> <p>aatag</p>
138	<p>GTGGTTGAAAAGAAAACTAAACCATACTTCAAGTTGATAATTGGAGGTGGGCAAAACAAG</p> <p>ACATTTGCTCCTGAAGAAAATTTCTGCAATGGTTCTACTAAAATGAAAGAAACCGCTGAG</p> <p>GCTTATTTGGGAAAAGAAG</p>
638	<p>ctaaatctctagaacaatcttaagtattttttctatcattagctattctcgggtggctgt</p>

- Oligo probes
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Exons/ Introns Translated sequence Flanking sequence Intron sequence UTR

Variants Downstream Frameshift Inframe deletion Inframe insertion Intronic Missense Splice donor Splice region

Stop gained Synonymous Upstream

Markup loaded

Show All entries Filter [Download what you see](#) [Download whole table](#)

Length	Sequence
326	<p>.....</p> <p>ACAGCACA</p> <p>CCTGTATT</p> <p>CCGCCTGC</p> <p>GCTGCTGC</p> <p>CTCAGCGC</p> <p>ATCGACCT</p>
97	<p>gtaagtgg</p> <p>gagggtgctgatgtccctctgtcgggtttttctgcag</p>
232	<p>CGTCGGGTGTTCAAGAACGGCCGCTGGAGATCATCGCAACGATCAGGGCAAACGCAT</p> <p>CACGCCGTCTATGTCGCCTCACTCCTGAAAGGGAAACGTCTGATGGGATGCCGCCAA</p> <p>GAACCAGCTCACCTCAACCCGAGAACACGGTCTTTGACGCCAAGGGCTCATGGCCG</p> <p>CAGGTGGAATGACCGTCTGTGCAGCAGGACATCAAGTTCTTGCCTTCAAG</p>
366	<p>gttcgaccgggtttttctcatccagttagagaacgggtgggtgggtggtgggagtatttagagt</p> <p>tataagtctctggaaaagtgttgagacaacagttgaaaggttatagacatgatgtatgtaa</p> <p>taactttaatactattagtatgttacaaaacttaagacagttgctgtcgtactgtctacg</p> <p>atagtttaggaataaaaagaccgattaaaactgaactttgtaagacacctatactccctga</p> <p>agtattctagtcaatttgcagcccaagggacaaaataaaccaaattgtgggagtggt</p> <p>agtgggtcttttaactttgagatgtcatgttatctgtgtctgaaaacaataattcttta</p> <p>aaatag</p>
138	<p>GTGGTTGAAAAGAAAACTAAACCATACATTCAAGTTGATAATTGGAGGTGGGCAAAACAAG</p> <p>ACATTTGCTCCTGAAGAAAATTTCTGCAATGGTTCTCACTAAAATGAAAAGAAACCGCTGAG</p> <p>GCTTATTTGGGAAAAGAAG</p>
638	<p>ctaaaatattctagaacaatcttaagtattttttctcatcattagtaattctcagttgactat</p>

Show/hide columns

- No.
- Exon / Intron
- Start
- End
- Start Phase
- End Phase
- Length
- Sequence

貼り付けのオプション:

- 形式を選択して貼り付け(S)...
- 既定の貼り付けの設定(A)...

ナビゲーション

文書の検索

見出し ページ 結果

文書に操作可能なアウトラインを作成します。

現在の位置がわかり、コンテンツを簡単に移動するのに便利です。

はじめに [ホーム] タブを選択して、文書の見出しに見出しスタイルを適用します。

本文 10.5 A Aa 挿入 A

段落

スタイル

あア亜 あア亜 あア亜 あア亜 あア亜

標準 行間詰め 見出し 1 見出し 2 表題

8 6 4 2 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48

326

ACAGCACAGACAGATTGACCTATTGGGGTGTTCGCGAGTGTGAGAGGGAAGC
 GCCGCGCCTGTATTTCTAGACCTGCCCTTCGCTGGTTCGTGGCGCCTTGTG
 ACCCCGGGCCCCTGCCGCCTGCAAGTCGGAAATTGCGCTGTGCTCCTGTGCTAC
 GGCCTGTGGCTGGACTGCCTGCTGCTGCCCAACTGGCTGGCAAGATGAAGCTC
 TCCCTGGTGGCCGCGATGCTGCTGCTGCTCAGCGCGGCGGGCCGAGGAGGA
 GGACAAGAAGGAGGACGTGGGCACGGTGGTCCGCATCGACCTGGGGACCACCT
 ACTCCTG

97

gtaagtggggttcggatgcagggggacggggcgctggccgctggcctggcgtgagaagtgcggtgctgatgtccctctgtcgggt
 tttctgccag

232

CGTCGGCGTGTTC AAGAACGGCCGCGTGGAGATCATCGCCAACGATCAGGGCAA
 CCGCATCACGCCGTCCTATGTGCGCTTCACTCCTGAAGGGGAACGTCTGATTGG
 CGATGCCGCCAAGAACCAGCTCACCTCCAACCCCGAGAACACGGTCTTTGACGC
 CAAGCGGCTCATCGGCCGACGTGGAATGACCCGTCTGTGCAGCAGGACATCAA
 GTTCTTGCCGTTCAAG

366

gttcgaccgggtttttctcatccagttagagaacgggtgggtgggtgggagtatttagagttataagtctctggaaaagtgttgagacia
 cagttgaaggttatagacatgatgtatgtaataactttaactatttagtatgttcaaaaacttaagacagttgctgctgactgtctacga
 tagtttaggaataaaaagaccgattaaaactgaactttgtaagacacctatactccctgaagtatttctagtcgaatttcagccccaagg
 accaaaataaaccaattgtggggatggtagtggtgcttttaactttgagatgtcattgtatctgtgctgaaaacaataattctttaa

ファイル ホーム 挿入 デザイン レイアウト 参考資料 差し込み文書 校閲 表示 EndNote 実行したい作業を入力してください...

游明朝 (本文) 10.5 A A Aa 7 冊 A

B I U abc x₂ x² A a/b A A (字)

あア亜 あア亜 あア亜 あア亜 あア亜

標準 行間詰め 見出し 1 見出し 2 表題

検索 置換 選択 編集

ナビゲーション

ATAAACCCAGATGAAGCTGTAGCG X

検索は一時停止しています

見出し ページ 結果

文書に操作可能なアウトラインを作成します。

現在の位置がわかり、コンテンツを簡単に移動するのに便利です。

はじめに [ホーム] タブを選択して、文書の見出しに見出しスタイルを適用します。

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38

8 6 4 2 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48

gtaaccatgtctttttctag

238

GATCTGTTCCGGTCTACTATGAAGCCCGTCCAGAAAGTGTGGAAGATTCTGAT
TTGAAGAAGTCTGATATTGATGAAATTGTTCTTGTTGGTGGCTCGACTCGAATT
CCAAAGATTCAGCAACTGGTTAAAGAGTTCTTCAATGGCAAGGAACCATCCCGT
GGCATAAACCCAGATGAAGCTGTAGCGTATGGTGCTGCTGTCCAGGCTGGTGT
GCTCTCTGGTGATCAAGATACAG **BiP-Fwd**

281

gtaggtcacatcgcagcatctttcttagtgattcagtagcttgatggaagactcattagctattgctttgaaaaataccagaatatgagc
aacaaggtcacacagctagtaaagggtataagtgagacaagactgggtagtctcaagatcattagcaactgttaattcactgcctt
taaaatgtgtgtgtagaacctaaccaaatgtagagagataaaactttacatagctcatagggagaactgaattaaagttaataact
tatecttacag

168

GTGACCTGGTACTGCTTGATGTATGTCCCCTTACACTTGGTATTGAAACTGTGG
GAGGTGTCATGACCAAAGTATTCCAAGGAACACAGTGGTGCCTACCAAGAAGT
CTCAGATCTTTTCTACAGCTTCTGATAATCAACCAACTGTTACAATCAAGGTCTA
TGAAG

986

gtaattacttaagttttaaatacatggcttttttttgagatgaagtcttctctgtgcccaggctggactgcagtggcacgatctcgg
ctcactgcaaattctgtctcccgggtcaagtattctctgcctcagcctcagagtagctgggattacaggcgtggaccaccacacc



Sequence Manipulation Suite: Version 2

<http://www.bioinformatics.org/sms2/index.html>

- Format Conversion
- Combine FASTA
- EMBL to FASTA
- EMBL Feature Extractor
- EMBL Trans Extractor
- Filter DNA
- Filter Protein
- GenBank to FASTA
- GenBank Feature Extractor
- GenBank Trans Extractor
- One to Three
- Range Extractor DNA
- Range Extractor Protein
- Reverse Complement
- Split Codons
- Split FASTA
- Three to One
- Window Extractor DNA
- Window Extractor Protein

- Sequence Analysis
- Codon Plot
- Codon Usage
- CpG Islands
- DNA Molecular Weight
- DNA Pattern Find
- DNA Stats
- Fuzzy Search DNA
- Fuzzy Search Protein
- Ident and Sim
- Multi Rev Trans
- Mutate for Digest
- ORF Finder
- Pairwise Align Codons
- Pairwise Align DNA
- Pairwise Align Protein
- PCR Primer Stats

- The Sequence Manipulation Suite is a collection of JavaScript programs for generating, formatting, and analyzing short DNA and protein sequences. It is commonly used by molecular biologists, for teaching, and for program and algorithm testing.
- See the [about the Sequence Manipulation Suite](#) page for more information about individual Sequence Manipulation Suite programs.
- You can easily [mirror the Sequence Manipulation Suite](#) on your own web site, or you can use it [off-line](#).
- This version of the Sequence Manipulation Suite represents a complete re-write of the previous version. The new version is much faster and has many new features. The [previous version](#) of the Sequence Manipulation Suite can still be accessed.
- Send questions and comments to stothard@ualberta.ca.

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- SMS
- Format Conversion
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Sequence Manipulation Suite: Reverse Complement

Reverse Complement converts a DNA sequence into its reverse, complement, or reverse-complement counterpart. The entire IUPAC DNA alphabet is supported, and the case of each input sequence character is maintained. You may want to work with the reverse-complement of a sequence if it contains an ORF on the reverse strand.

Paste the raw sequence or one or more FASTA sequences into the text area below. Input limit is 100,000,000 characters.

```
>BiP-Rev  
GGACATACATCAAGCAGTACCAGG
```

Submit Clear Reset

• reverse-complement

*This page requires JavaScript. See [browser compatibility](#).
*You can [mirror this page](#) or use it off-line.

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Sequence Manipulation Suite - Mozilla Firefox

ファイル(E) 編集(E) 表示(V) 履歴(S) ブックマーク(B) ツール(T) ヘルプ(H)

www.bioinformatics.org/sms2/rev_comp.html

Reverse Complement results

```
>BiP-Rev reverse complement
CCTGGTACTGCTTGATGTATGTC
```

copy

counterpart. The entire IUPAC DNA alphabet is supported, and the
ent of a sequence if it contains an ORF on the reverse strand.

0,000 characters.

ナビゲーション

CCTGGTACTGCTTGATGTATGTCC x

検索は一時停止しています

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gtaaccatgtctttttctag
238
GATCTGTTCCGGTCTACTATGAAGCCCGTCCAGAAAGTGTGGAAGATTCTGAT
TTGAAGAAGTCTGATATTGATGAAATTGTTCTTGTGTTGGTGGCTCGACTCGAATT
CCAAAGATTCAGCAACTGGTTAAAGAGTTCTTCAATGGCAAGGAACCATCCCGT
GGCATAAACCAGATGAAGCTGTAGCCATGGTGCTGCTGTCCAGGCTGGTGT
GCTCTCTGGTGATCAAGATACAG **BiP-Fwd**
281
gtaggatcatcatcgagcatctttcttagtgattcagtagcttgatggaagactcattagctattgctttagaaaataccagaatatgagc
aacaagggtcacacagctagtaaagggtataagtgagacaagactgggtagtctcaagatcattagcaactgttaattcactgcctt
taaaatgtgtgttagaacctaaccataatgtagagagataaaactttacatagctcatagggagaactgaattaaagttaaataact
tatecttacag
BiP-Rev
168
GTGACCTGGTACTGCTTGATGTATGTCCCTTACACTTGGTATTGAACTGTGG
GAGGTGTCATGACCAAAGTATTCCAAGGAACACAGTGGTGCCTACCAAGAAGT
CTCAGATCTTTTCTACAGCTTCTGATAATCAACCAACTGTTACAATCAAGGTCTA
TGAAG
986
gtaattacttaagttttaaataatcatggcttttttttgagatgaagctctgtgcccaggctggactgcagtgccacgatctcgg
ctcactgcaaattctgtctcccgggttaagtgattctctgcctcagcctccagagtagctgggattacaggcgtggaccaccacacc



Points of Primer design for real-time PCR

1. Use Primer design software.
2. Primer length: 17 to 25 bases. GC content: 45% to 55%.
3. Amplicon length: 80-150bp.
4. Primers should not anneal with themselves on 3' ends.
5. Primers should be separated by long intron(s) if possible.
6. Same T_m values for both primers is preferred.
7. Avoid T on 3' end of the primers if possible (G or C is better).