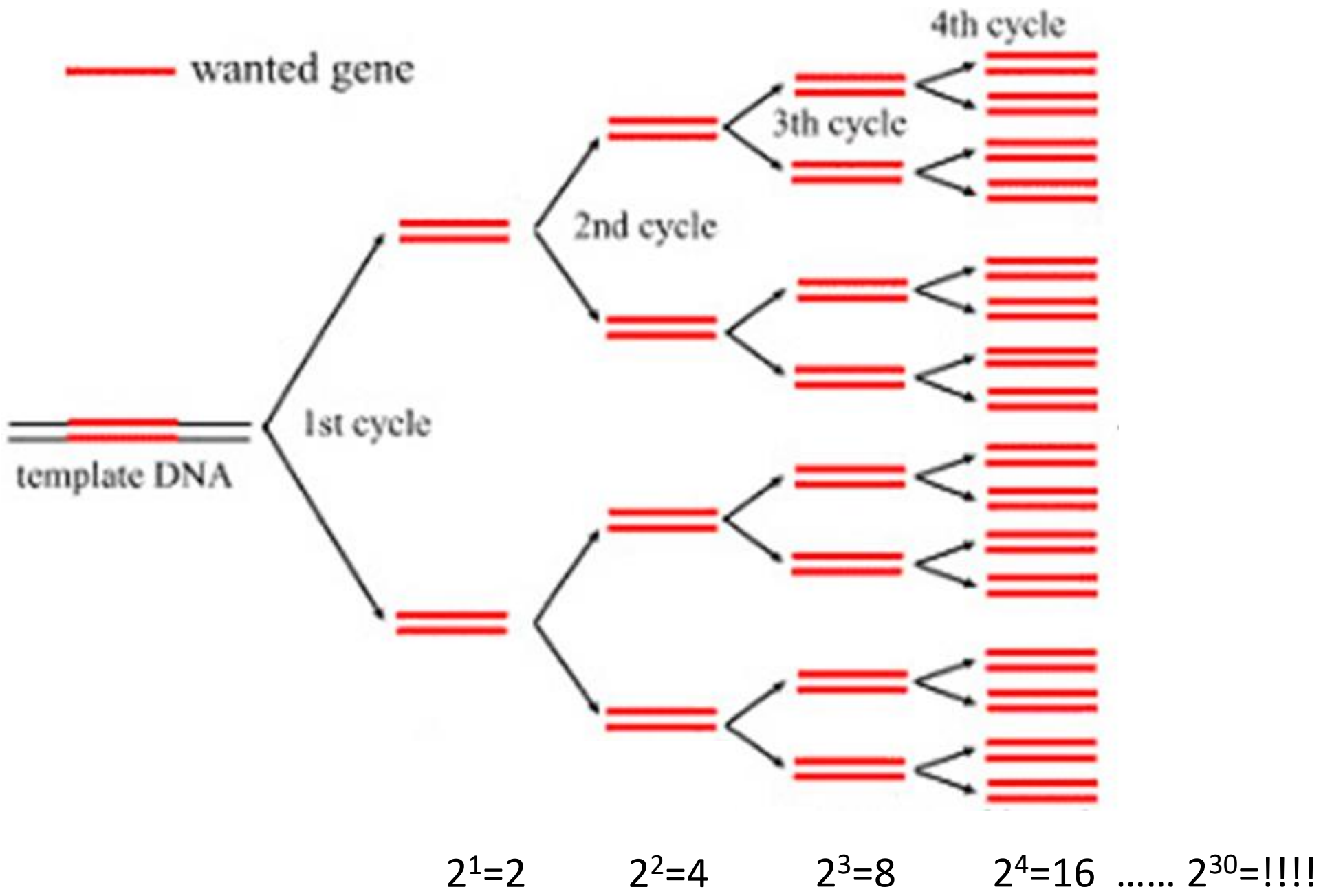
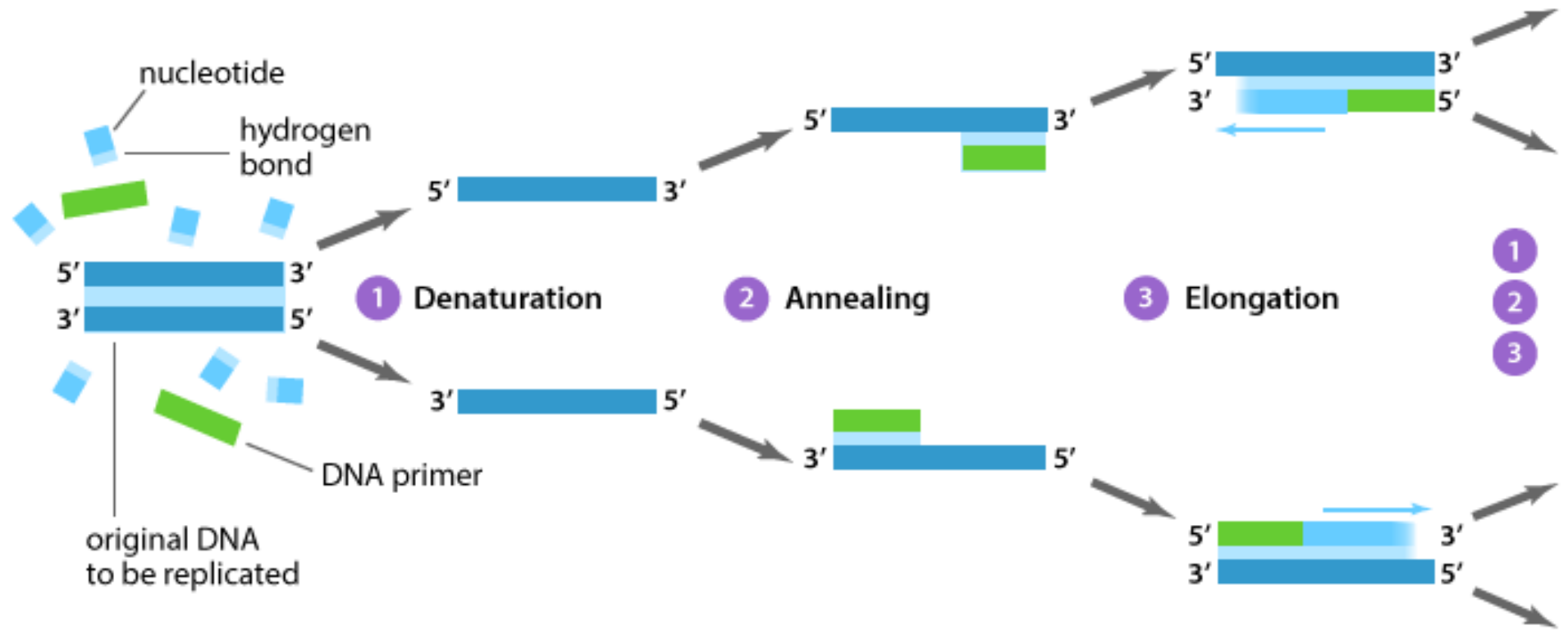


PCR & primer orientation

- sense primer
- antisense primer
- Annhyb for primers
- [Primer3](#)





5' ..aggtcatccggttatctagacataatagatctagatcgtccgatcgtacgt...3'
3' ..tccagttaggcaatagatctgtattatctagatctagcaggctagcatgca...5'

Please design primers to amplify this region.

sense primer = ?
antisense primer = ?

5' ..aggtc**atccg**ttatctagacataatagatctagatcgtccgatcgtacgt...3'
3' ..tccag**taggca**atagatctgtattatctagatctagcaggctagcatgca...5'



DENATURATION

5' ..aggtc**atccg**ttatctagacataatagatctagatcgtccgatcgtacgt...3'

3' ..tccag**taggca**atagatctgtattatctagatctagcaggctagcatgca...5'

sense primer = 5'- -3'
antisense primer = 5'- -3'

Only for teaching purposes - not for reproduction or sale

5' ..aggtcatccgttatctagacataatagatctagatcgtccgatcgtacgt...3'
3' ..tccagtaggcaatagatctgtattatctagatctagcaggctagcatgca...5'



DENATURATION

5' ..aggtcatccgttatctagacataatagatctagatcgtccgatcgtacgt...3'

3' ..tccagtaggcaatagatctgtattatctagatctagcaggctagcatgca...5'

sense primer = 5'-catccgtta-3'
antisense primer = 5'-tacgatcgg-3'

5' .. aggtcatccgttatctagacataatagatctagatcgtccgatcgtacgt...3'
3' .. tccagtaggcaatagatctgtattatctagatctagcaggctagcatgca...5'



DENATURATION

5' -catccgtta-3'

3' -ggctagcat-5'

5' .. aggtcatccgttatctagacataatagatctagatcgtccgatcgtacgt...3'
3' -ggctagcat-5'

ANNEALING

5' -catccgtta-3'
3' .. tccagtaggcaatagatctgtattatctagatctagcaggctagcatgca...5'

sense primer = 5'-catccgtta-3'
antisense primer = 5'-tacgatcgg-3'

Only for teaching purposes - not for reproduction or sale

5' .. aggtcatccgttatctagacataatagatctagatcgtccgatcgtacgt...3'
3' .. ggctagcat-5'

ELONGATION

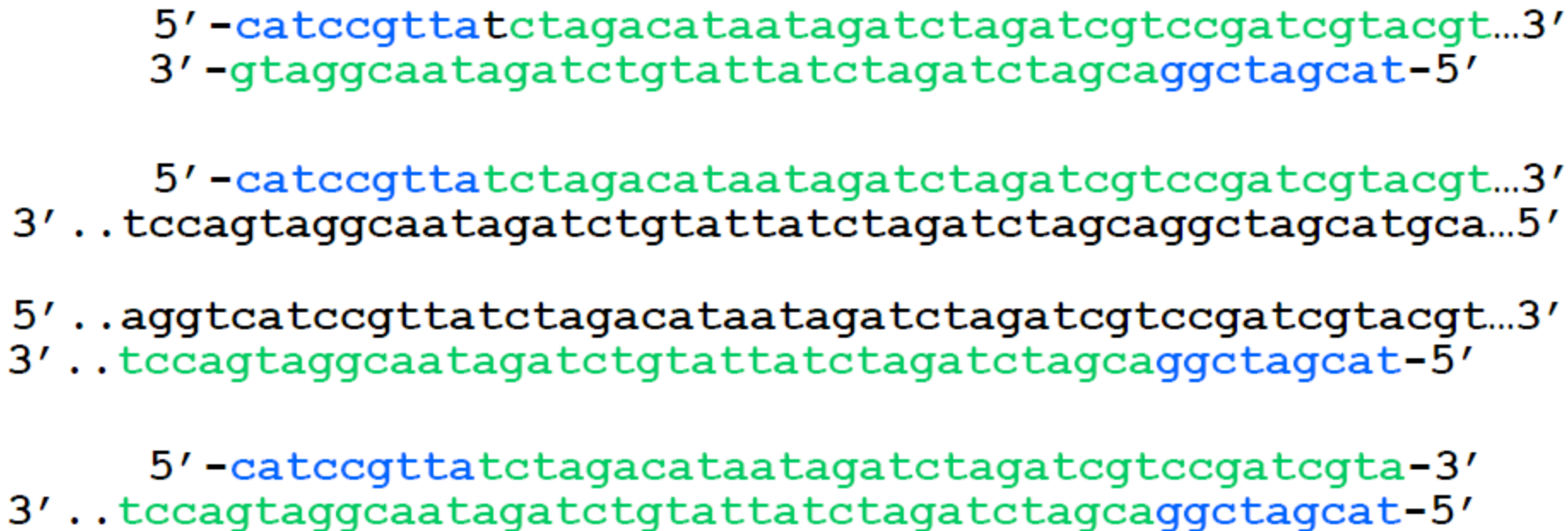
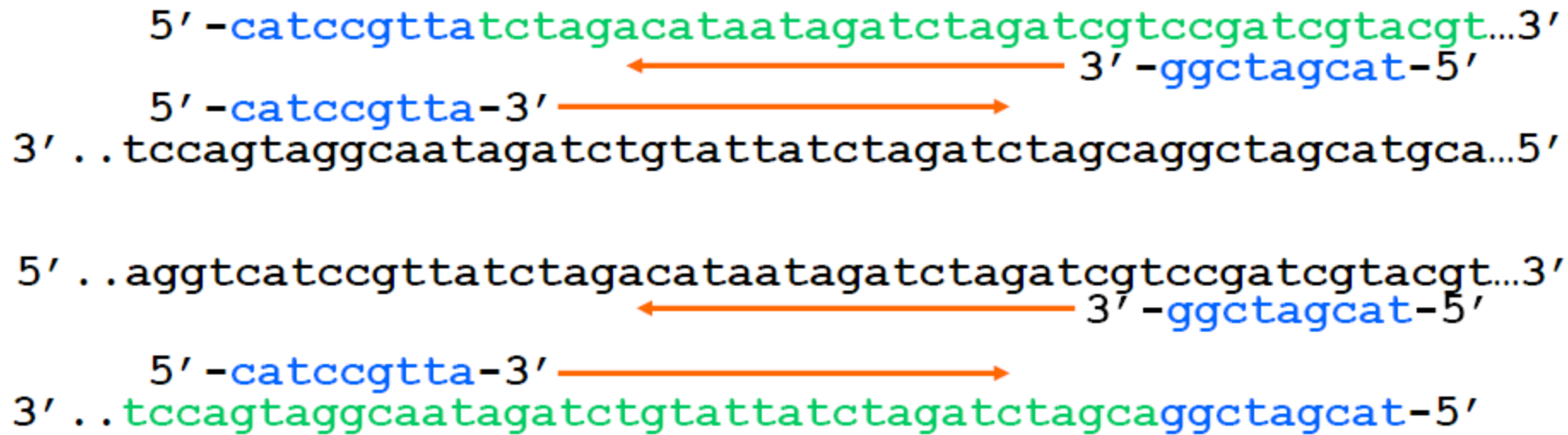
5' - catccgtta-3'
3' .. tccagtaggcaatagatctgtattatctagatctagcaggctagcatgca...5'



5' .. aggtcatccgttatctagacataatagatctagatcgtccgatcgtacgt...3'
3' .. tccagtaggcaatagatctgtattatctagatctagcaggctagcat-5'

5' - catccgttatctagacataatagatctagatcgtccgatcgtacgt...3'
3' .. tccagtaggcaatagatctgtattatctagatctagcaggctagcatgca...5'





You have to amplify ALL the following sequence, from the first to the last nucleotide; please design the FORWARD (=SENSE) primer, 12 base pair long (the REVERSE/ANTISENSE primer is requested in the following question).

5-ATGAAGCTGGCGACGGGACTGTTTGGTGGCAGCCAGGACCGTC-3

3-TACTTCGACCGCTGCCCTGACAAACCACCGTCGGTCCTGGCAG-5

Write only nucleotides, not symbols or numbers.

Answer:

You have to amplify ALL the following sequence, from the first to the last nucleotide; please design the REVERSE (=ANTISENSE) primer, 12 base pair long (the FORWARD/SENSE primer is requested in the previous question).

5-ATGAAGCTGGCGACGGGACTGTTTGGTGGCAGCCAGGACCGTC-3

3-TACTTCGACCGCTGCCCTGACAAACCACCGTCGGTCCTGGCAG-5

Write only nucleotides, not symbols or numbers.

Answer:

You have to amplify ALL the following sequence, from the first to the last nucleotide; please design the FORWARD (=SENSE) primer, 12 base pair long (the REVERSE/ANTISENSE primer is requested in the following question).

5-ATGAAGCTGGCGACGGGACTGTTTGGTGGCAGCCAGGACCGTC-3

Write only nucleotides, not symbols or numbers.

Answer:

You have to amplify ALL the following sequence, from the first to the last nucleotide; please design the REVERSE (=ANTISENSE) primer, 12 base pair long (the FORWARD/SENSE primer is requested in the previous question).

5-ATGAAGCTGGCGACGGGACTGTTTGGTGGCAGCCAGGACCGTC-3

Write only nucleotides, not symbols or numbers.

Answer:

```

/moi_type= mRNA
/strain="BDIX"
/db_xref="taxon:10116"
/cell_line="JS1 schwannoma"
/note="cell line derived from a peripheral nerve sheath
tumor induced by in utero treatment with nitrosoethylurea"
1..2540
/gene="Nrg1"
370..2457
/gene="Nrg1"
/note="sensory and motor neuron-derived factor splice
variant; cysteine-rich domain neuregulins; growth and
differentiation factor"
/codon_start=1
/product="SMDF neuregulin alpha 2a"
/protein_id="AAG28428.1"
/translation="MEIYSPDMSEVAGGRSSSPSTQLSAVPSLDGLPAAEEHIPDHT
EDERSPGLLGLAVPCCVCLEAERLRGCLNSEKICIVPILACLVSCLCIAGLKWVFD
KIFEYDSPTHLDPGGLGQDPVISLDPATAAPAILVSSEAYTSPVSKAQSEAGAHVTVQG
DHAAVASEPSAVPTRKNRLSAFPPFHPTAPPFPSPARTPEVRTPKSGTQPQTETNLQ
TAPKLSTSTSTTGTSHLIKAEKEKTCVNGGECFTVKDLSNPSRYLCKCQPGFTGAR
CTENVPMKVQTQEKAEELYQKRVLTIITGICIALLVVGIMCVVAYCKTKKQRQKLHDL
RQSLRSERSNLVNIANGPHHPNPPENVQLVNVQYVSKNVISSEHIVEREVETSFSSTSH
YTSTAHSTTTVTQTPSHSWSNGHTESVISESNSVIMMSSVENSRRHSSPAGGPRGRLHG
LGGPRDNSFLRHARETPDSYRDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMS
PPVSSMTVSMPSVAVSPFVEEERPLLLVTPPRLREKKYDHHPPQLNSFHHPAHQSTS
LPPSPLRIVEDEEYETTQEYESVQEPVKKVTNSRRAKRTKPNGHIANRLEMSNTSSV
SSNSESETEDERVGEDTPFLGIQNPLAASLEVAPAFRLAESRTNPAGRFSTQEELQAR
LSSVIANQDPIAV"

```

[gene](#)
[CDS](#)

If I ask you to amplify the cDNA starting from ATG, where do you put the sense primer?

ORIGIN

```

1 gaattoggca cgaggcggca gcttgcttcc tattttggtc ccoctgccttc ttgaccaacc
61 cggcatggtt tggagaagca tttgaaagaa ctgaaaaagt gtcccagaaa caacagctca
121 agatatttcg gtacacttct atttcatagt tgctagaagc cctttctttt ttogtttttt
181 ttttttcttt ttctttttct ttttcttttt ccttttcttg ctctctccta agctctggta
241 ctttgggtaa ttgccttgga cttgggtgcc ttatcgattt cccctccaa gatgctgtat
301 catttggttg gggggagctc tgcgtggtaa tgcactgtga gagaggccag gccttctgga
361 ggtgagccga tggagattta ttccccagac atgtctgagg tagctggcgg gaggtcctcc
421 agcccccca ctcagctgag tgcagttcca tctcttgatg ggcttccggc agcggaggaa
481 catataccag acaccacac agaagatgag agaagccctg gactcctggg cctggcggtg

```

```
/mgi_type= mRNA
/strain="BDIX"
/db_xref="taxon:10116"
/cell_line="JS1 schwannoma"
/note="cell line derived from a peripheral nerve sheath
tumor induced by in utero treatment with nitrosoethylurea"
1..2540
/gene="Nrg1"
370..2457
/gene="Nrg1"
/note="sensory and motor neuron-derived factor splice
variant; cysteine-rich domain neuregulins; growth and
differentiation factor"
/codon_start=1
/product="SMDF neuregulin alpha 2a"
/protein_id="AAG28428.1"
/translation="MEIYSPDMSEVAGGRSSSPSTQLSAVPSLDGLPAAEEHIPDHT
EDERSPGLLGLAVPCCVCLEAERLRGCLNSEKICIVPILACLVSCLCIAGLKWVFD
KIFEYDSPHTLDPGGLGQDPVISLDPTAAPAILVSSEAYTSPVSKAQSEAGAHVTVQG
DHAAVASEPSAVPTRKNRLSAFPFHTAPFPSPARTPEVRTPKSGTQPQTETNLQ
TAPKLSTSTSTTGTSHLIKAEKEKTCVNGGECFTVKDLSNPSRYLCKCQPGFTGAR
CTENVPMKVQTQEKAEELYQKRVLTIITGICIALLVVGIMCVVAYCKTKKQRQLHDRL
RQSLRSERSNLVNIANGPHHPNPPENVLVNQYVSKNVISSEHIVEREVETSFSTSH
YTSTAHHSTTVTQTPSHSWSNGHTESVISESNSVIMMSSVENSRRHSSPAGGPRGRLHG
LGGPRDNSFLRHARETPDSYRDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMS
PPVSSMTVSMPSVAVSPFVEEERPLLLVTPPRLREKKYDHPQQLNSFHHPAHQSTS
LPPSPLRIVEDEEYETTQEYESVQEPVKKVTNSRRAKRTKPNGHIANRLEMSNTSSV
SSNSESETEDERVGEDTPFLGIQNPLAASLEVAPAFRLAESRTNPAGRFSTQEELQAR
LSSVIANQDPIAV"
```

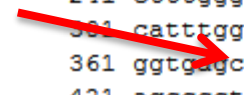
gene
CDS



If I ask you to amplify the cDNA starting from ATG, you have to identify the first ATG (the "start codon") of the coding sequence!

ORIGIN

```
1 gaattoggca cgaggcggca gcttgcttcc tattttggtc ccoctgccttc ttgaccaacc
61 cggcatgggt tggagaagca tttgaaagaa ctgaaaaagt gtcccagaaa caacagctca
121 agatatttcg gtacacttct atttcatagt tgctagaagc cctttctttt ttogtttttt
181 ttttttcttt ttctttttct ttttcttttt ccttttctctg cttcctccta agctctggta
241 ctttgggtaa ttgccttgga cttgggtgcc tttatcgatt ccccctccaa atgctgtat
301 catttggttg gggggagctc tgcgtggta atgactgtga gagaggccag gccttctgga
361 ggtgagccca tggagattta ttccccagac atgtctgagg tagctggcgg gaggtcctcc
421 agccccctca ctcagctgag tgcagttcca tctcttgatg ggcttccggc agcggaggaa
481 catataccag acaccacac agaagatgag agaagcctg gactcctggg cctggcggtg
```



<http://bioinformatics.org/annhyb/>

AnnHyb

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AnnHyb is a tool for working with and managing nucleotide sequences in multiple formats.

The features include sequence viewer, sequence editor, sequence annotation, format conversion, oligonucleotides alignment, restriction analysis, pattern s multi-alignment viewer, consensus determination, etc.

AnnHyb runs under **Microsoft-Windows** (NT4, 2000, XP, Vista, 7)

A version of AnnHyb also running under **Linux** and **Mac OSX** is available at [PyAnnHyb](#)

AnnHyb is **free software**, and is released under the GNU **General Public License**.

If you find it useful, please [send me](#) a nice postcard

Please send your comments and/or suggestions at [annhyb @ gmail .com](mailto:annhyb@gmail.com)

Current version: 4.946 [what's new?](#)

Others programs for bioinformatic

- [FASTA/BLAST Scan](#): processing of FASTA and BLAST outputs

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How to use Annhyb to design primers

File Edit Oligo Sequence Multiple alignment Help

(c) Olivier Friard 1997-2008

Oligo | Oligo list | Sequence | Sequence list | Multi-alignment | Multi-alignment list

Name: Sequence1 Long name:

Description:

Length: 5712 Type: DNA checksum: 9812 Author: Creation date: 27/10/2012

Sequence header:

Sequence annotations

Name	init	end	comments

1 gaattcggca cgaggcgatg ctcagagggc
 51 tgattcagcc tctttcagcc gctgcgttaa
 101 actgtcgctg ctgectctcc tgccgccgcc
 151 ctctgggtctt gcttttgctt ttactttctcc
 201 cctctaagca gacaccagct tcagacgctt gaggtgagaa acatgccttt
 251 cagtttgga tactggttta cttaatcggc tagggggcag cttgcttcc
 301 atttgggtcc cctgccttct tgaccaaccc ggcatggttt ggagaagcat
 351 ttgaaagaac tgaaaaagtg tcccagaaac aacagctcaa gatatttcgg
 401 tacacttcta ttccatagtt gctagaagcc ctttcttttt cgtttttttt
 451 ttctttttct ttttcttttt ctttttctt ttcctgcttc ctccaaagct
 501 ctggtacttt ggtaattgc cttggacttg ggtgccttat cgatttcccc
 551 ctccaagatg ctgtatcatt tggttggggg gagctctgcg tggtaatgca
 601 ctgtgagaga ggccaggcct tctggaggtg agccgatgga gattttattcc
 651 ccagacatgt ctgaggtagc tggcggggagg tcctccagcc cctccactca
 701 gctgagtgca gccccatctc ttgatgggct tccggcagcg gaggaacata
 751 taccagacac ccacacagaa gatgagagaa gccctggact cctgggctg
 801 ggggtgccct gctgtgtgtg cctggaagct gagcgctga gaggggtgtct
 851 caactccgag aagatctgca ttgttcccat tctggcttgc ctagtccagcc
 901 tctgcctctg cattgctggc ctgaagtggg tatttgtgga caagatattt
 951 gaatacgact ctccatccca ccttgaccct ggggggttag gccaggaccc
 1001 tgtgatttct ctggatccaa ctgctgcccc agccattttg gtatcatctg
 1051

Seq. length: 5712 Selection: 151 - 174 (24 bp) Tm= 55.0°C (Allawi, 1997)

Confirm

Copy only nucleotides?

Yes No

File Edit **Oligo** Sequence Multiple alignment Help

New oligo
 Import oligo in project
 Remove oligo(s)
 Export
 Print
 Test oligo for dimers and hairpin loops
 Quick search oligo in sequences
 Align oligo with sequences
 Quick search oligo in multiple alignment
 Align oligo in multiple alignment

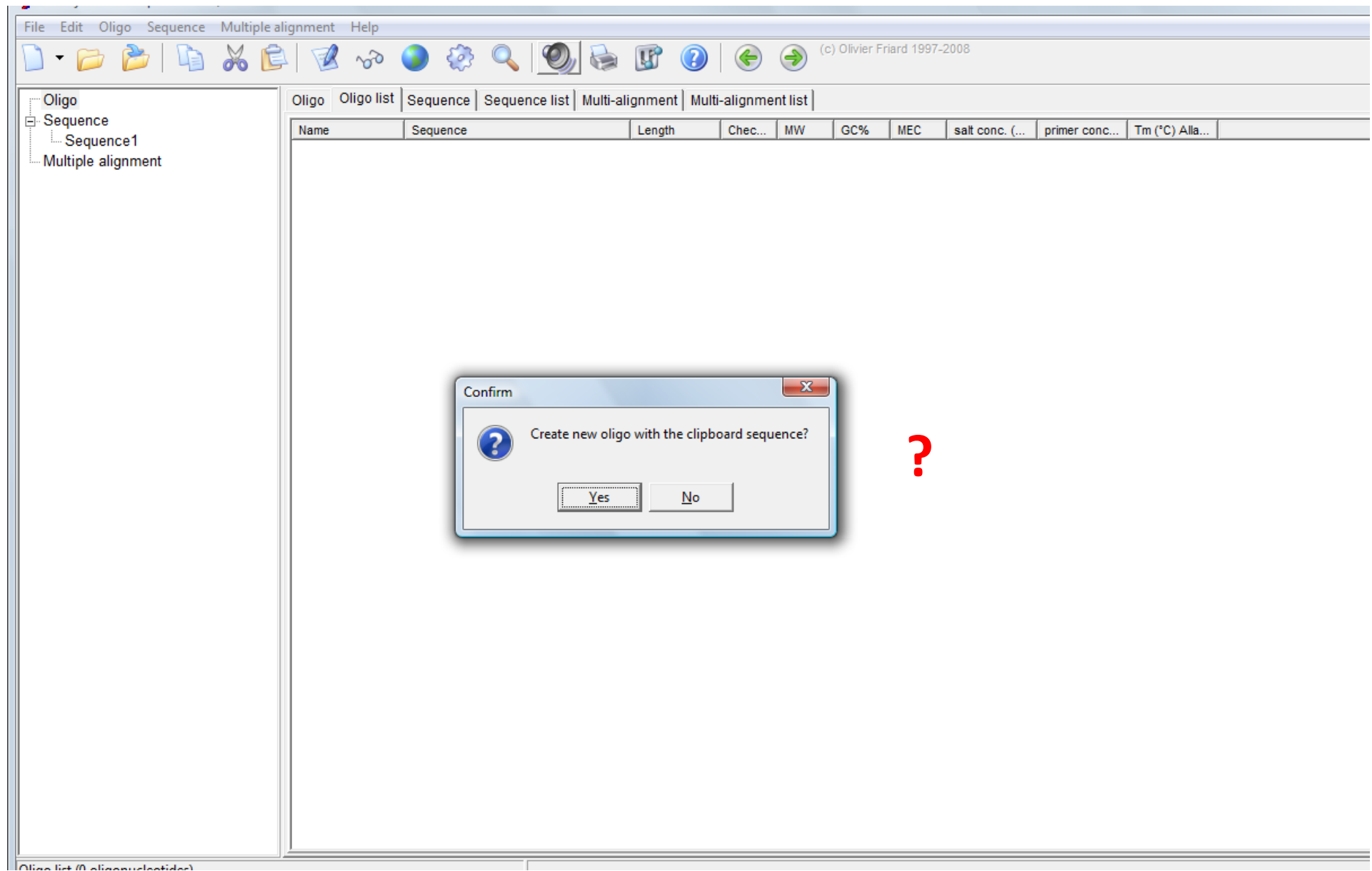
Sequence | Sequence list | Multi-alignment | Multi-alignment list

Sequence 1 Long name

Type DNA checksum 9812 Author Creation date 27/10/2012

	name	init	end	comments	
1	gaattcggca	cgaggcgatg	ctcagagggc	aggcacctgc	tgctctgtaa
51	tgattcagcc	tctttcagcc	gctgogttaa	cacgacagga	tgctgttgct
101	actgtgcgtg	ctgcctctcc	tgccgcccgc	gctgctgccc	ccgcccgcctc
151	ctctggctct	gcttttgctt	ttactctccc	tgcatgacag	ttgttttctt
201	cctctaagca	gacaccagct	tcagacgctt	gaggtgagaa	acatgccttt
251	cagtttggga	tactggttta	cttaatcggc	taggcggcag	cttgcttcct
301	atthtgggtcc	cctgccttct	tgaccaaccc	ggcatggttt	ggagaagcat
351	ttgaaagaac	tgaaaaagtg	tcccagaaac	aacagctcaa	gatatttcgg
401	tacacttcta	ttccatagtt	gctagaagcc	ctttcttttt	cgtttttttt
451	ttctttttct	ttttcttttt	cttttctctt	ttctgcttc	ctcctaagct
501	ctggtacttt	gggtaattgc	cttggaactg	ggtgccttat	cgatttcccc
551	ctccaagatg	ctgtatcatt	tggttggggg	gagctctcgc	tggtaatgca
601	ctgtgagaga	ggccaggcct	tctggagggtg	agccgatgga	gatttatctc
651	ccagacatgt	ctgaggtagc	tggcgggagg	tcctccagcc	cctccactca
701	gctgagtgca	gccccatctc	ttgatgggct	tcggcagcg	gaggaacata
751	taccagacac	ccacacagaa	gatgagagaa	gccctggact	cctgggcctg
801	gcggtgcctc	gctgtgtgtg	cctggaagct	gagcgcctga	gaggggtctc
851	caactccgag	aagatctgca	tgtttcccat	tctggcttgc	ctagtcagcc
901	tctgcctctg	cattgctggc	ctgaagtggg	tatttggtga	caagatattt
951	gaatacgact	ctcctaccca	ccttgaccct	gggggggttag	gccaggacct
1001	tgtgatttct	ctggatccaa	ctgctgcccc	agccattttg	gtatcatctg

Seq. length: 5712 Selection: 151 - 174 (24 bp) Tm= 55.0°C (Allawi, 1997)



File Edit Oligo Sequence Multiple alignment Help

(c) Olivier Friard 1997-2008

Oligo | Oligo list | Sequence | Sequence list | Multi-alignment | Multi-alignment list

Name: notes None

Seq. 5' Insert the sequence of oligo

IUB seq.5'

rev. 5'

comp.

Length	MW	GC%	GCG checksum	Molar ext. coef.
24 b	7320	41.6%	3134	198360 /mol (at 280 nm)

Salt cc mM Primers cc nM Tm °C

Alignment results Allawi, 1997

Seq. name	sense	init	end	score	alignment	Sequence target	Color ...

Insert the sequence of oliao

primer sense
(create oligo with the clipboard sequence)

primer antisense
(DO NOT create oligo with the clipboard sequence, you have to copy and paste the sequence here, to obtain the reverted and complementary correct primer!!)

5' -catccgтта-3'

5' .. aggtcatccgттatctagacataatagatctagatcgtccgatcgtacgt...3'
 3' .. tccagtaggcaatagatctgtattatctagatctagcaggctagcatgca...5'

3' -ggctagcat-5'

Pay attention! The sequence in Annhyb is single strand! When you copy it to obtain the antisense primer you need to revert and complement it!

5' .. aggtcatccgттatctagacataatagatctagatcgtccgatcgtacgt...3'

File Edit Oligo Sequence Multiple alignment Help

New oligo
 Import oligo in project
 Remove oligo(s)
 Export
 Print
 Test oligo for dimers and hairpin loops
 Quick search oligo in sequences
 Align oligo with sequences
 Quick search oligo in multiple alignment
 Align oligo in multiple alignment

Sequence | Sequence list | Multi-alignment | Multi-alignment list

Sequence name: ce1 Long name:

Type: DNA checksum: 9812 Author: Creation date: 27/10/2012

Name	init	end	comments
1	gaattcggca	cgaggcgatg	ctcagagggc
51	tgattcagcc	tctttcagcc	gctgcgtaa
101	actgtcgcctg	ctgcctctcc	tgccgcgcc
151	ctctgggtctt	gcttttgctt	ttacttctcc
201	cctctaagca	gacaccagct	tcagacgctt
251	cagtttggga	tactggttta	cttaatcggc
301	attttggtcc	cctgccttct	tgaccaacc
351	ttgaaagaac	tgaaaaagtg	tcccagaaac
401	tacacttcta	ttcatagtt	gctagaagcc
451	ttctttttct	tttcttttt	ctttttcctt
501	ctggtacttt	gggtaattgc	cttggacttg
551	ctccaagatg	ctgtatcatt	tggtggggg
601	ctgtgagaga	ggccaggcct	tctggagggtg
651	ccagacatgt	ctgaggtagc	tggcgggagg
701	gctgagtgca	gccccatctc	ttgatgggct
751	taccagacac	ccacacagaa	gatgagagaa
801	gcggtgccct	gctgtgtgtg	cctggaagct
851	caactccgag	aagatctgca	ttgttcccat
901	tctgcctctg	cattgctggc	ctgaagtggg
951	gaatacgact	ctoctaccca	ccttgaccct
1001	tgtgatttct	ctggatccaa	ctgctgcccc

Seq. length: 5712 Selection: 151 - 174 (24 bp) Tm= 55.0°C (Allawi, 1997)

Pay attention! The sequence in Annhyb (and in ncbi) is single strand!

5' .. aggtcatccgttatctagacataatagatctagatcgtccgatcgtacgt...3'

The screenshot shows the Oligo software interface. The menu bar includes File, Edit, Oligo, Sequence, Multiple alignment, and Help. The toolbar contains icons for file operations, a settings gear, a search magnifying glass, a printer, a help question mark, and navigation arrows. A red arrow points to the settings gear icon. A context menu is open over the settings icon, listing the following options: Test oligo for dimers and hairpin loops, Restriction analysis, Translate sequence, Reverse/complement sequence, Find ORF, Base composition, Codon usage, Crypt/Decrypt sequence, PCR product, and Melting temperature.

The left sidebar shows a tree view with the following items: Oligo (expanded), Oligo1-sense (selected), Oligo1-antisense, Oligo1, Oligo2, Sequence, Sequence1, and Multiple alignment.

The main window displays the following data:

Name	Oligo1-se		
Seq. 5'	CTCTGGTCT		
IUB seq.5'	CTC TGG T		
rev. comp. 5'	GTAAAAGCA		
Length	MW		
24	b	732	
Salt cc	50	mM	Prim

Alignment results table:

Seq. name	sense	init	end	score	alignment	Sequence target	Color ...

File Edit Oligo Sequence Multiple alignment Help

(c) Olivier Friard 1997-2008

Oligo | Oligo list | Sequence | Sequence list | Multi-alignment | Multi-alignment list

Name: notes None

Seq. 5'

IUB seq.5'

rev. 5'

comp.

Length	MW	GC%	GCG checksum	Molar ext. coef.
24	b 7320	41.66	3134	198360 /mol (at 260 nm)

Salt cc mM Primers cc nM Tm °C

Alignment results Allawi, 1997

Seq. name	sense	init	end	score	alignment	Sequence target	Color ...

Primer dimers and Hairpin loops

Oligo1-sense: CTCTGGTCTTGCTTTTGCTTTTAC
 Oligo1-sense : CTCTGGTCTTGCTTTTGCTTTTAC
 Oligo1-antisense : TGCCGCTAGCCGATTAAG

Dimers < > Max

```

CTCTGGTCTTGCTTTTGCTTTTAC
|  |  |  |  |
CAATTCGTTTCGTTCCTGGTCTC
    
```

Hairpin loops < > Max

```

      CTCTGGTC
      |  |  |  T
CAATTCGTTTCGT
    
```

? Save Close

File Edit Oligo Sequence Multiple alignment Help

(c) Olivier Friard 1997-2008

Oligo | Oligo list | Sequence | Sequence list | Multi-alignment | Multi-alignment list

Name notes None

Seq 5'

UUB seq.5'

rev. 5'

comp.

Length	MW	GC%	GCG checksum	Molar ext. coef.
24 b	7320	41.6%	3134	198360 /mol (at 280 nm)

Salt cc mM Primers cc nM Tm °C

Alignment results Allawi, 1997

Seq. name	sense	init	end	score	alignment	Sequence target	Color ...
-----------	-------	------	-----	-------	-----------	-----------------	-----------

Primer dimers and Hairpin loops

Oligo1-sense: CTCTGGTCTTGCTTTTGCTTTTAC

Oligo1-sense : CTCTGGTCTTGCTTTTGCTTTTAC

Oligo1-antisense : TGCCGCTAGCCGATTAAG

Dimers < > Max

```

CTCTGGTCTTGCTTTTGCTTTTAC
  ||  ||
GAATTAGCCGATCCGCGT

```

Hairpin loops < > Max

```

CTCTGGT
 |  |  T
CAITTCGTTTCGT

```

? Save Close

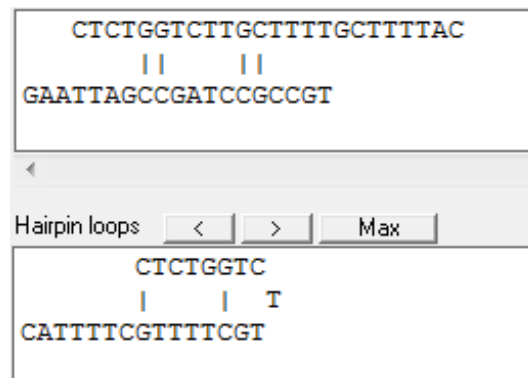
* primer pairs must meet the following criteria:

1- to have similar Tm (about 60°C according to Allawi: 59-61°C)

2- to finish with G or C

3- to have a content of G and C \geq 50%

4- not to form secondary structures (use Annhyb: tools -> test for dimers and hairpin loops). Test each primer against itself and against the other primer: you want to have \leq 5 consecutive pairings: if you have \geq 6 you have to design new primers



File Edit **Oligo** Sequence Multiple alignment Help

(c) Olivier Friard 1997-2008

Sequence | Sequence list | Multi-alignment | Multi-alignment list

Sequence	Length	Chec...	MW	GC%	MEC	salt conc. (...)	primer conc...	Tm (°C) Alla...
CTCTGGTCTTGCTTTTGCTTTTAC	24	3134	7320	41.7	198360	50	250	55.0
TGCCGCCTAGCCGATTAAG	19	3490	5851	57.9	179190	50	250	56.5

... Oligo
... Oligo
Sequ...
Seq...
Multiple

- New oligo
- Import oligo in project
- Remove oligo(s)
- Export
- Print
- Test oligo for dimers and hairpin loops
- Quick search oligo in sequences
- Align oligo with sequences**
- Quick search oligo in multiple alignment
- Align oligo in multiple alignment

AnnHyb 4.943 September 09, 2010

File Edit Oligo Sequence Multiple alignment Help

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Oligo

- Oligo1-sense
- Oligo1-antisense

 Sequence

- Sequence1

 Multiple alignment

Oligo list | **Sequence** | Sequence list | Multi-alignment | Multi-alignment list

Name	Sequence	Length	Chec...	MW	GC%	MEC	salt conc. (...)	primer conc...	Tm (°C) Alla...
<input checked="" type="checkbox"/> ■ Oligo1-sen...	CTCTGGTCTTGCTTTTGCTTTTAC	24	3134	7320	41.7	198360	50	250	55.0
<input checked="" type="checkbox"/> ■ Oligo1-anti...	TGCCGCCTAGCCGATTAAG	19	3490	5851	57.9	179190	50	250	56.5

Microsoft PowerPoint - [291012.ppt]

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File Edit Oligo Sequence Multiple alignment Help

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Oligo | Oligo list | Sequence | Sequence list | Multi-alignment | Multi-alignment list

Name: Sequence1 Long name:

Description:

Length: 5712 Type: DNA checksum: 9812 Author: Creation date: 27/10/2012

Sequence header:

Sequence annotations

Name	init	end	comments
■ Oligo1-sense	151	174	found oligo score: 100 sense: ...
■ Oligo1-antisense	271	289	found oligo score: 100 sense: ...

```

1  gaattcggca cgaggcgatg ctacagagggc aggcacctgc tgctctgtaa
51  tgattcagcc tctttcagcc gctgogtaa cacgacagga tgctgttgct
101 actgtcgctg ctgcctctcc tgccgcggcc gctgctgccc cgcgcgcctc
151 ctctgggtctt gcttttgctt ttactttctc tgcattgacag ttgttttctt
201 cctctaagca gacaccagct tcagacgctt gaggtgagaa acatgccttt
251 cagtttggga tactggttta cttaatcggc tagggcgcag cttgcttctc
301 attttggtcc cctgccttct tgaccaaccg gccatggttt ggagaagcat
351 ttgaaagaac tgaaaaagtg tcccagaaac aacagctcaa gatatttcgg
401 tacacttota ttcatagtt gctagaagcc ctttcttttt cgtttttttt
451 ttctttttct ttttcttttt ctttttctct ttctctgctc ctcttaagct
501 ctggtaactt ggtaattgc cttgacttgg ggtgccttat cgatttcccc
551 ctccaagatg ctgtatcatt tggttggggg gagctctgog ttgtaatgca
601 ctgtgagaga ggccaaggct tctggagggt agccgatgga gatttatcc
651 ccagacatgt ctgaggtagc tggcggggag tcctccagcc cctccactca
701 gctgagtgca gccccatctc ttgatgggct tccggcagcg gaggaacata
751 taccagacac ccacacagaa gatgagagaa gccctggact cctgggcctg
801 gcggtgcccct gctgtgtgtg cctggaagct gagcgcctga gaggggtgct
851 caactccgag aagatctgca ttgttccat tctggcttgc ctagtacgac
901 tctgcctctg cattgctggc ctgaagtggg tatttgtgga caagatattt
951 qaatacqaact ctctaccaca ccttqaccct aaaaaattaa acaaaqacc

```

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File Edit Oligo Sequence Multiple alignment Help

(c) Olivier Friard 1997-2008

Oligo | Oligo list | Sequence | Sequence list | Multi-alignment | Multi-alignment list

Name: Sequence1 Long name:

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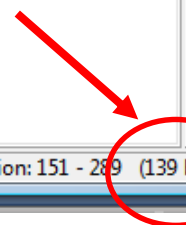
```

1  gaattcggca cgaggcgatg ctcagagggc aggcacctgc tgctctgtaa
51  tgattcagcc tctttcagcc gctgcgttaa cacgacagga tgctgttgct
101 actgtcgcct ctgectctcc tgccgcgcgc gctgctgccc ccgcgcgcctc
151 ctctgggtctt gcttttgctt ttactttctcc tgcatgacag ttgttttctt
201 cctctaagca gacaccagct tcagacgctt gaggtgagaa acatgccttt
251 cagtttggga tactggttta cttaatcggc taggcggcag cttgcttcc
301 attttggtec cctgccttct tgaccaaccc ggcattggtt ggagaagcat
351 ttgaaagaac tgaaaaagt tccagaaac aacagctcaa gatatttcgg
401 tacacttcta tttcatagtt gctagaagcc ctttctttt cgttttttt
451 ttctttttct tttctttt ctttttctt ttctgcttc ctctaagct
501 ctggtacttt gggtaattgc cttggacttg ggtgccttat cgatttccc
551 ctccaagatg ctgtatcatt tggttggggg gagctctgcg tggtaatgca
601 ctgtgagaga ggccaggcct tctggaggtg agccgatgga gatttatcc
651 ccagacatgt ctgaggtagc tggcgggagg tcctccagcc cctccactca
701 gctgagtgca gcccatctc ttgatgggct tcggcagcg gaggaacata
751 taccacacac ccacacaaa atatgagaaa cccttqact cctqaaacct

```

Seq. length: 5712 Selection: 151 - 289 (139 bp) m= 75.2°C (Howley, 1979)

Length of the
amplification
product



PCR & primer orientation

- sense primer
- antisense primer
- Annhyb for primers
- [Primer3](#)

[Load server settings:](#)

Default

Activate Settings

Select primer pairs to detect the given template sequence. Optionally targets and included/excluded regions can be specified.

[Task:](#)

generic

Pick Primers

Reset Form

Main**General Settings****Advanced Settings****Internal Oligo****Penalty Weights****Advanced Sequence**[Sequence Id:](#)[Paste template sequence below](#)Or upload sequence file: Nessun file selezionato.

Mark selected region:

[Excluded Regions:](#)

<

>

[Targets:](#)

[

]

[Included Region:](#)

{

}

[Primer overlap positions:](#)

-

[Pair OK Region List:](#)

News: Try out our new tool: [Wiley-DNA-Editor](#) - A DNA/Plasmid editor running in your browser!

Primer3Plus

pick primers from a DNA sequence

[More...](#)[Source Code](#)[Help](#)[About](#)

[Load server settings:](#)

Select primer pairs to detect the given template sequence. Optionally targets and included/excluded regions can be specified.

[Task:](#)

[Main](#)[General Settings](#)[Advanced Settings](#)[Internal Oligo](#)[Penalty Weights](#)[Advanced Sequence](#)

[Product Size Ranges:](#)

Primer Size

[Min:](#)

[Opt:](#)

[Max:](#)

Primer Tm

[Min:](#)

[Opt:](#)

[Max:](#)

[Max Tm Difference:](#)

Primer GC%

[Min:](#)

[Opt:](#)

[Max:](#)

[Concentration of monovalent cations:](#)

[Annealing Oligo Concentration:](#)

[Concentration of divalent cations:](#)

[Concentration of dNTPs:](#)

[Mispriming/Repeat Library:](#)

Load and Save

To upload or save a settings file from your local computer, choose here:

Nessun file selezionato.