

Gene sequence and primer design



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What is primer?



Primer design for diagnosis and regular amplification

- Previous experiments
- Software
- By hand



How to design your Primer

Free software

<http://frodo.wi.mit.edu/primer3/>

http://www.humgen.nl/primer_design.html

Many others

Gene sequence

Pubmed

<http://www.ncbi.nlm.nih.gov>

Omp25 *Brucella*

```
gene      1..642
          /gene="omp25"
CDS       1..642
          /gene="omp25"
          /codon_start=1
          /product="outer membrane protein 25"
          /protein_id="CAQ68393.1"
          /db_xref="GI:206596726"
          /db_xref="GOA:B5U6Y0"
          /db_xref="InterPro:IPR011250"
          /db_xref="UniProtKB/TrEMBL:B5U6Y0"
          /translation="MRTLKSLVIVSAALLPFSATAFAADAIQEQQPPVPAPVEVAPQYS
WAGGYTGLYLGYGWNKAKTSTVGSIKPDDWKAGAFAGWNFQQDQIVYGVEGDAGYSWA
KKSKDGLLEVKGQFEGSLRARVGYDLNPVMPYLTAGIAGSQIKLNGLDDESKFRVGWT
AGAGLEAKLTDNILGRVEYRYTQYGNKNYDLAGTNVRNKLDTQDIRVGIGYKF"

ORIGIN
    1 atgcgcactc ttaagtctct cgtaatcgtc tcggctgcgc tgctgccggt ctctgcgacc
   61 gcttttgctg ccgacgccat ccaggaacag cctccgggtc cggctccggt tgaagtagct
  121 cccagttata gctgggctgg tggctatacc ggtctttacc tcggctacgg ctggaacaag
  181 gccaagacca gcaccgttgg cagcatcaag cctgacgatt ggaaggctgg cgcttttgct
  241 ggctggaact tccagcagga ccagatcgta tatggtgttg aaggatgatc aggttattcc
  301 tgggccaaga agtccaagga cggcctggaa gtcaagcagg gctttgaagg ctgcgtgcgt
  361 gccgcgctcg gctacgacct gaaccgggtt atgccgtacc tcacggctgg tattgccggt
  421 tcgcagatca agcttaacaa cggcttggac gacgaaagca agttccgcgt gggttggacg
  481 gctggtgccg gtctcgaagc caagctgacg gacaacatcc tcggccgcgt tgagtaccgt
  541 tacaccagt acggcaacaa gaactacgat ctggccggta cgaatgtccg caacaagctg
  601 gacacgcagg atatccgcgt cggcatcggc tacaagttct aa

//
```

WebPrimer software



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Web Primer: DNA and Purpose Entry

Sequences of **primer sets** available to the community

DNA Source [\[info\]](#)

Locus: Enter a standard gene name or systematic ORF name (i.e. ACT1, YKR054C)

OR

Enter the DNA Sequence (numbers are OK, but comments should be removed)

Purpose: PCR or Sequencing [\[info\]](#)

☒ **PCR** [\[info\]](#) or
☐ **SEQUENCING** [\[info\]](#)

Copy and paste sequence

copy

```
/db_xref="GOA:B5U6Y0"  
/db_xref="InterPro:IPR011250"  
/db_xref="UniProtKB/TrEMBL:B5U6Y0"  
/translation="MRTLKSLVIVSAALLPFSATAFAADAIQEQQPPVPAPVEVAPQYS  
WAGGYTGLYLGYGWNKAKTSTVGSIKPDDWKAGAFAGWNFQQDQIVYGVEGDAGYSWA  
KKSKDGLEVKQGFEGLSLRVRVGYDLNPFVMPYLTAGIAGSQIKLNNGLDDESKFRVGT  
AGAGLEAKLTDNII LGRVEYRYTQYGNKNYDLAGTNVRNKLDTQDIRVGIGYKF"  
  
ORIGIN  
1 atgcgcactc ttaagtctct cgtaaatcgtc tcggctgcgc tgctgcccgtt ctctgcgacc  
61 gctttttgctg ccgacgcccac ccaggaacag cctccgggttc cggctccgggt tgaagtagct  
121 ccccagttata gctgggctgg tggctatacc ggtctttacc tcggctacgg ctggaacaag  
181 gccaaagacca gcaccggttg cagcatcaag cctgacgatt ggaaggctgg cgcttttctg  
241 ggctggaaact tccagcagga ccagatcgta tatgggtgtg aagggtgatgc aggttattcc  
301 tgggccaaga agtccaagga cggcctggaa gtcaagcagg gctttgaagg ctgctgcgt  
361 gcccgctgog gctacgaact gaacccgggt atgcogtacc tcacggctgg tattgcoggt  
421 tcgcagatca agcttaacaa cggcttggac gacgaaagca agttccgctg gggttggacg  
481 gctggtgccc gtctcgaagc caagctgacg gacaacatcc tcggccgctg tgagtaccgt  
541 tacaccaggt acggcaacaa gaactacgat ctggccggta cgaatgtccg caacaagctg  
601 gacacgcagg atatccgctg cggcatcggc tacaagttct aa  
//
```

paste

Sequences of primer sets available to the community

DNA Source [\[info\]](#)

Locus: Enter a standard gene name or systematic ORF name (i.e. ACT1, YKR054C)

OR

Enter the DNA Sequence (numbers are OK, but comments should be removed)

```
481 gctgggtgccg gtctcgaagc caagctgacg gacaacatcc tcggccgctg  
tgagtaccgt  
541 tacaccaggt acggcaacaa gaactacgat ctggccggta cgaatgtccg  
caacaagctg  
601 gacacgcagg atatccgctg cggcatcggc tacaagttct aa
```

Purpose: PCR or Sequencing [\[info\]](#)

- ☒ PCR [\[info\]](#) or
☐ SEQUENCING [\[info\]](#)

Submit

Reset

Options to choose from!

Location [\[info\]](#)

Select YES to Amplify a region with **EXACT** endpoints of the DNA sequence entered ☒ NO ☐ YES

Length of DNA in which to search for valid primers:

Melting Temperature [\[info\]](#)

Optimum Tm: Minimum Tm: Maximum Tm:

Optimum primer length: Minimum length: Maximum length:

Primer Composition [\[info\]](#)

Optimum percent GC content: Minimum GC: Maximum GC:

Primer Annealing [\[info\]](#)

Self Anneal: Self End Anneal: Pair Anneal: Pair End Anneal:

Primers for PCR

There were 66 forward primers in the valid range for GC content.
There were 23 reverse primers in the valid range for GC content.
There were 43 forward primers in the valid range for melting temperature.
There were 22 reverse primers in the valid range for melting temperature.
There were 43 forward primers with valid self anneal values.
There were 22 reverse primers with valid self anneal values.
There were 33 forward primers with valid self end anneal values.
There were 22 reverse primers with valid self end anneal values.
Some primers were not evaluated

There were 250 pairs of valid primers.

This is the BEST pair of primers

List of all valid pairs of primers

Best choice of primer pair

Primer Pair Data

Primers for 1 (Entered)

These primers are for PCR

Forward-Primer	ATGCGCACTCTTAAGTCTCT	Reverse-Primer	TTAGAACTTGTAGCCGATGCC
Length:	20	Length:	21
Percent GC:	45	Percent GC:	47
Tm:	48	Tm:	53
Self-Anneal:	20	Self-Anneal:	10
End-Anneal:	6	End-Anneal:	4
Offset:	1	Offset:	642

Pair-Anneal: 16

Pair-End-Anneal: 8

Total valid primer pairs: 250

These primers will amplify a fragment of 642 basepairs

The sequence of DNA that will be amplified by these primers is

```

1  ATGCGCACTC TTAAGTCTCT CGTAATCGTC TCGGCTGCGC TGCTGCCGTT
51 CTCTGCGACC GCTTTTGCTG CCGACGCCAT CCAGGAACAG CCTCCGGTTC
  
```

Things to avoid in Primer Design

A primer may be self-complementary and fold into a **hairpin**:

5-GTTGACTTGATATTATCAAG-3

**5'-GTTGACTTGATA
 |||||T
3'-GAACTAT**

Things to avoid in Primer Design

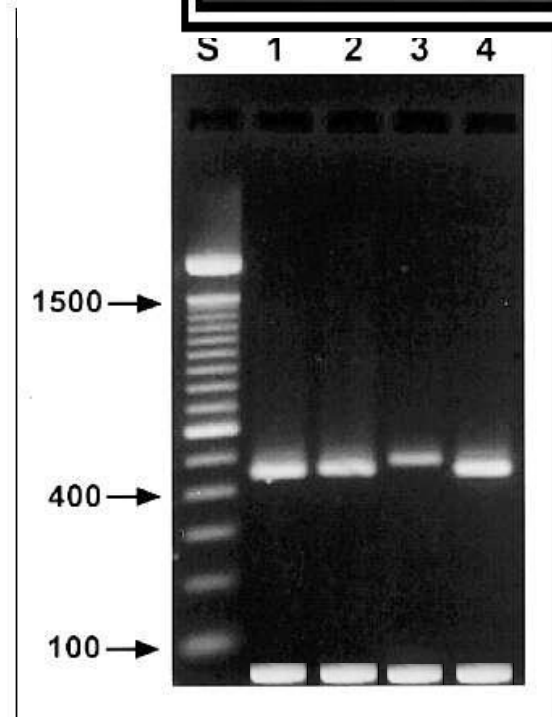
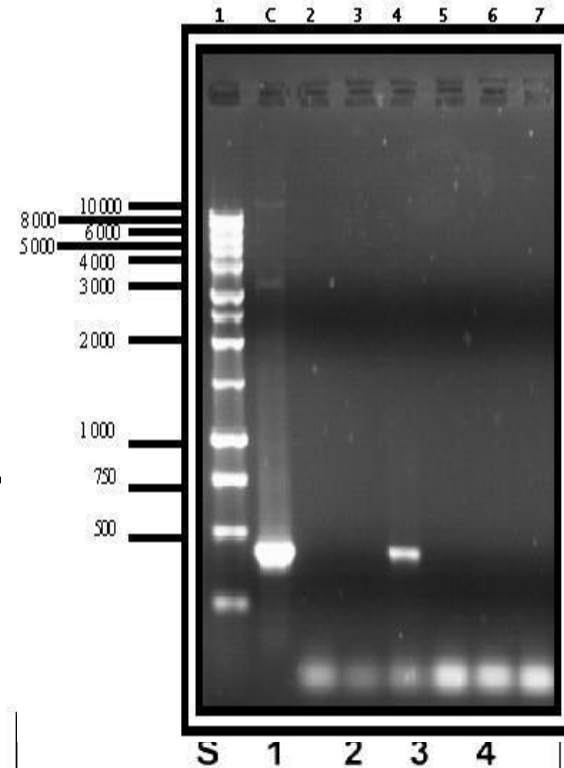
A primer may form a **dimer** with itself or with the other primer.

5'-ACCGGTAGCCACGAATTCGT-3'

5'-ACCGGTAGCCACGAATTCGT-3'

|||||

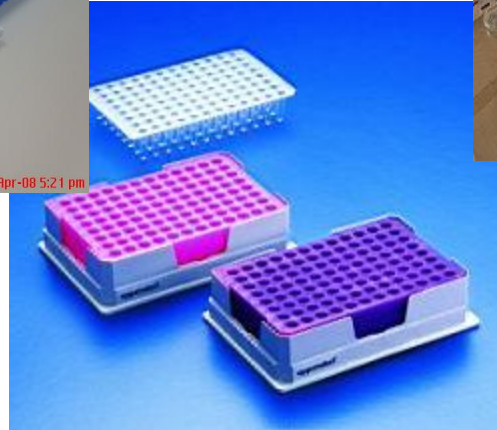
3'-TGCTTAAGCACCGATGGCCA-5'



Order primers commercially

- 3.5 - 4 Egyptian Pounds for base
- Powder
- 5,000 reactions

Set up PCR reaction



Set up PCR reaction



Reagents in a tube

1- 5 μ l (200 ng)

1 μ l F and 1 μ l R 20 pmol

25 μ l – 50 μ l

- Sample (DNA)

- Primers (forward and reverse)

- Enzyme (DNA polymerase, *Taq*)

- dNTPs (A, T, G, C)

- Buffer (50 mM KCl; 10 mM Tris-HCl; 1.5 mM MgCl₂)

If needed

- Water DNAase free water

Thermocycler



PCR Cycles

Time and temperature

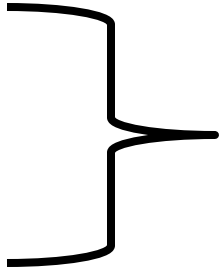
- Initial denature

- denature

- annealing

- extension

- Final extension



25-40 cycles



PCR Cycles

Time and Temperature

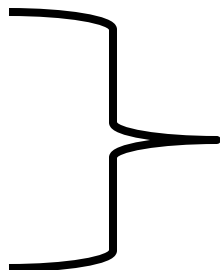
- Initial denature

94 °C for 2-5 minuets

- denature

- annealing

- Extension



25-40 cycles

94 °C for 30 sec

55 °C for 30 sec

68-72 °C for xxx sec

- Final extension

72 °C for 5 minuets

Overnight Thermocycler



Last step incubation

- 10 °C for gene cloning
- Room temperature for diagnosis

How to chose your enzyme And your company

taq vs pfu

Diagnosis vs molecular cloning

Promega GoTaq green mastermix (cat no. M7122)

Qiagen mastermix

DNA Polymerase

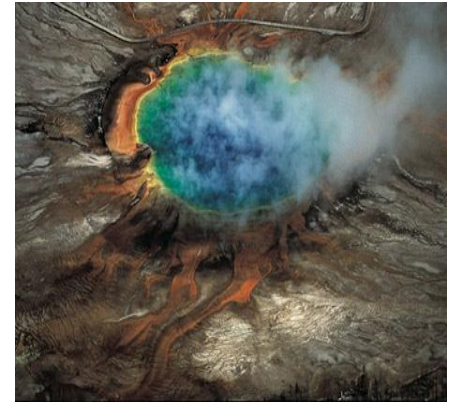
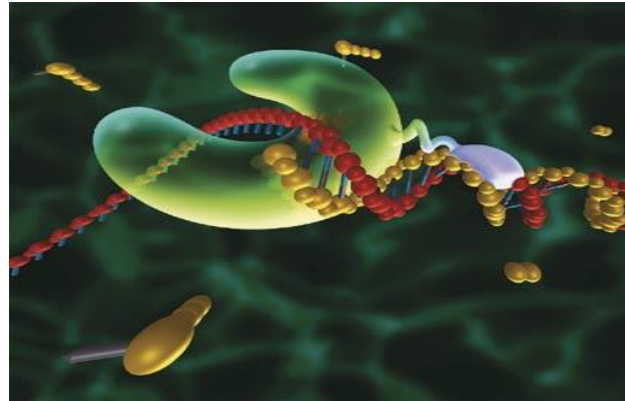
Thermus aquaticus

Taq enzyme

Heat stable

1988

Error 1:10,000



Hot spring

Pyrococcus furiosus

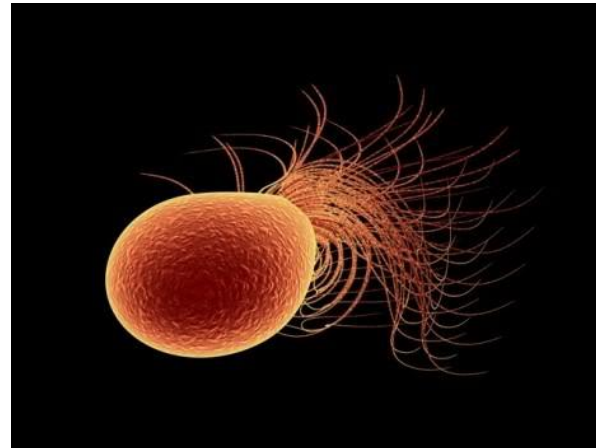
Pfu enzyme

More stable

1991

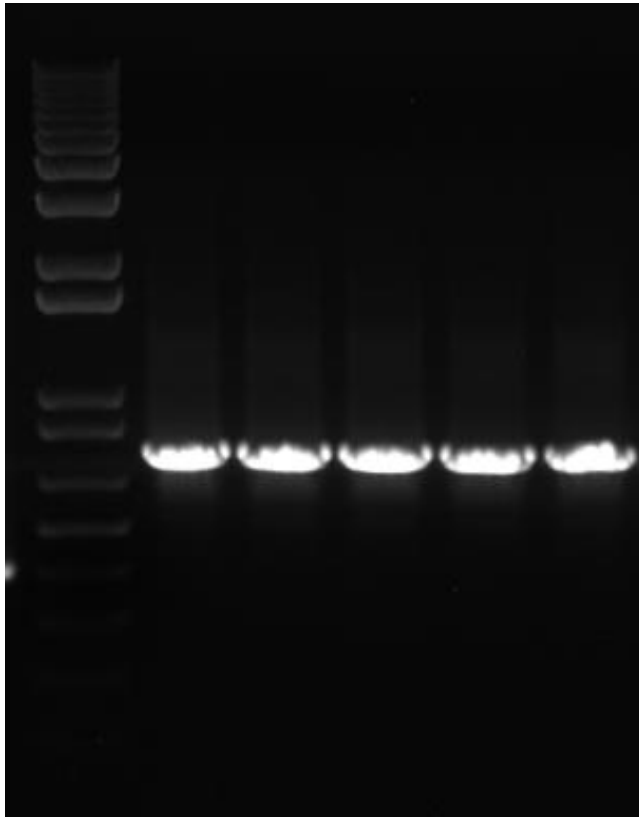
Error 1: Million

3' to 5' exonuclease proofreading activity



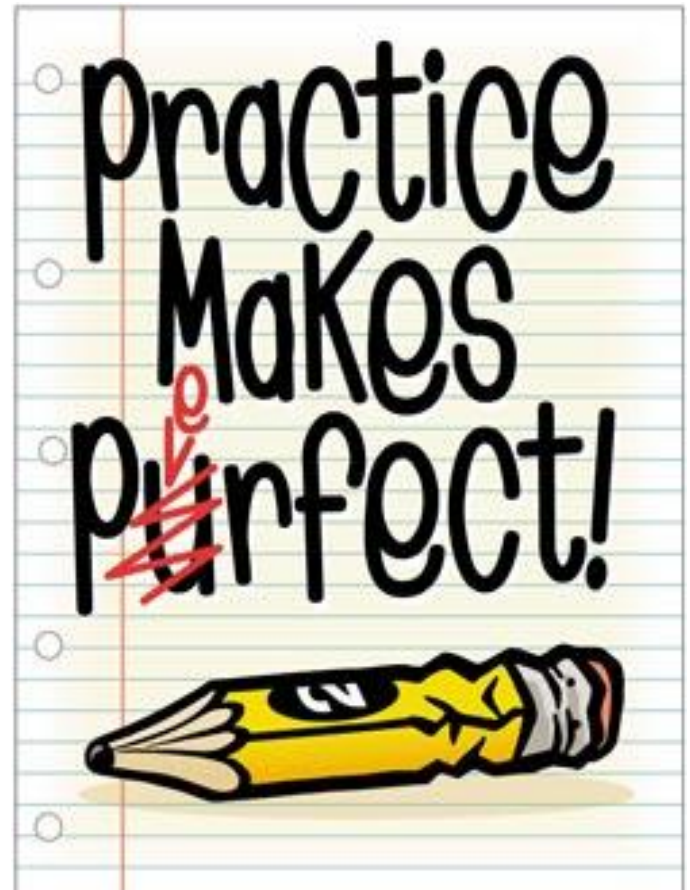
Marker

PCR products

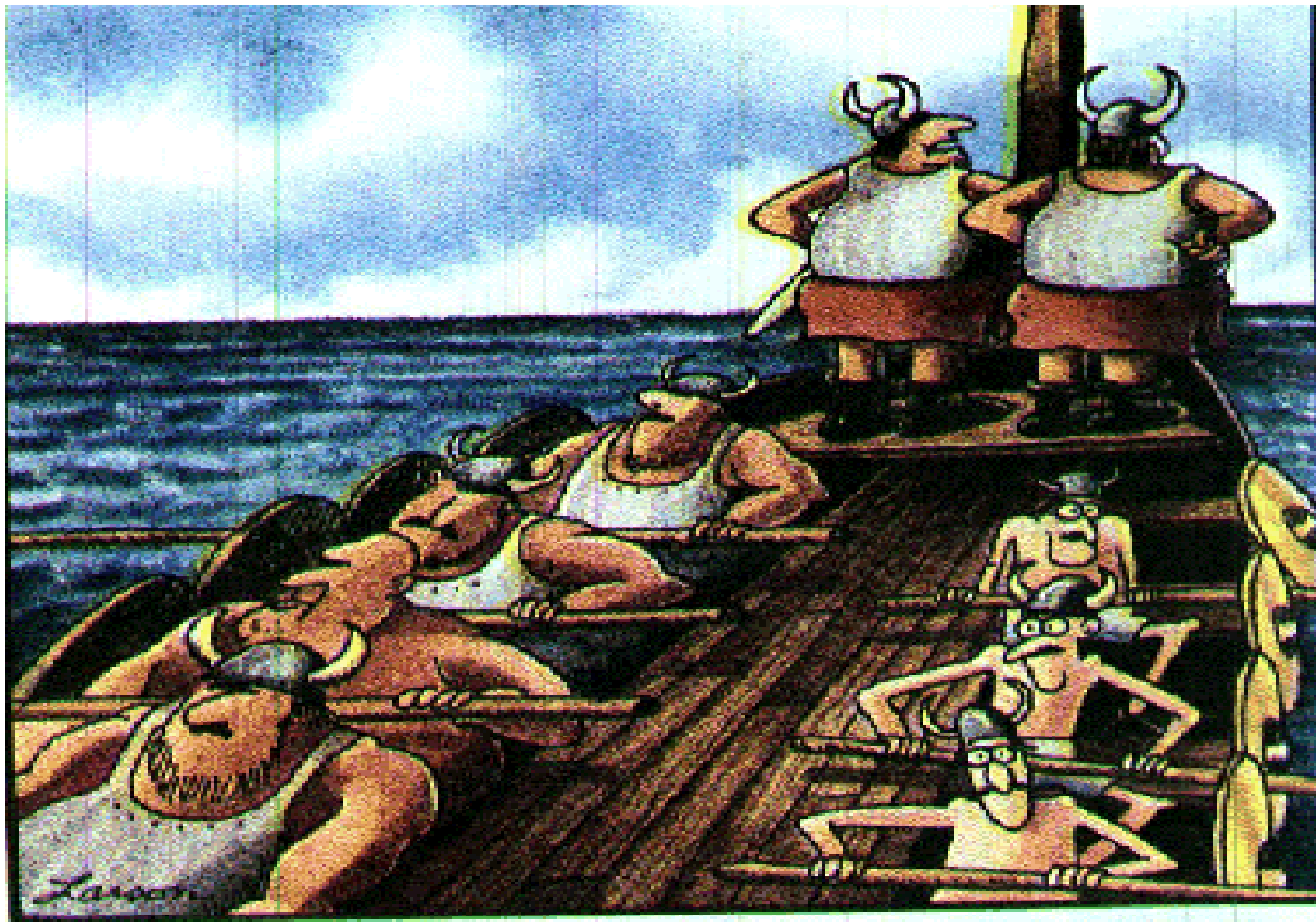


Real time PCR

Needs practice



Questions!!!



"I've got it, too, Omar ... a strange feeling like we've just been going in circles."