



[www.esaunggul.ac.id](http://www.esaunggul.ac.id)

# PENGANTAR BIOINFORMATIKA

## IBT 431

*By Seprianto S.Pi, M.Si*

Pertemuan 6

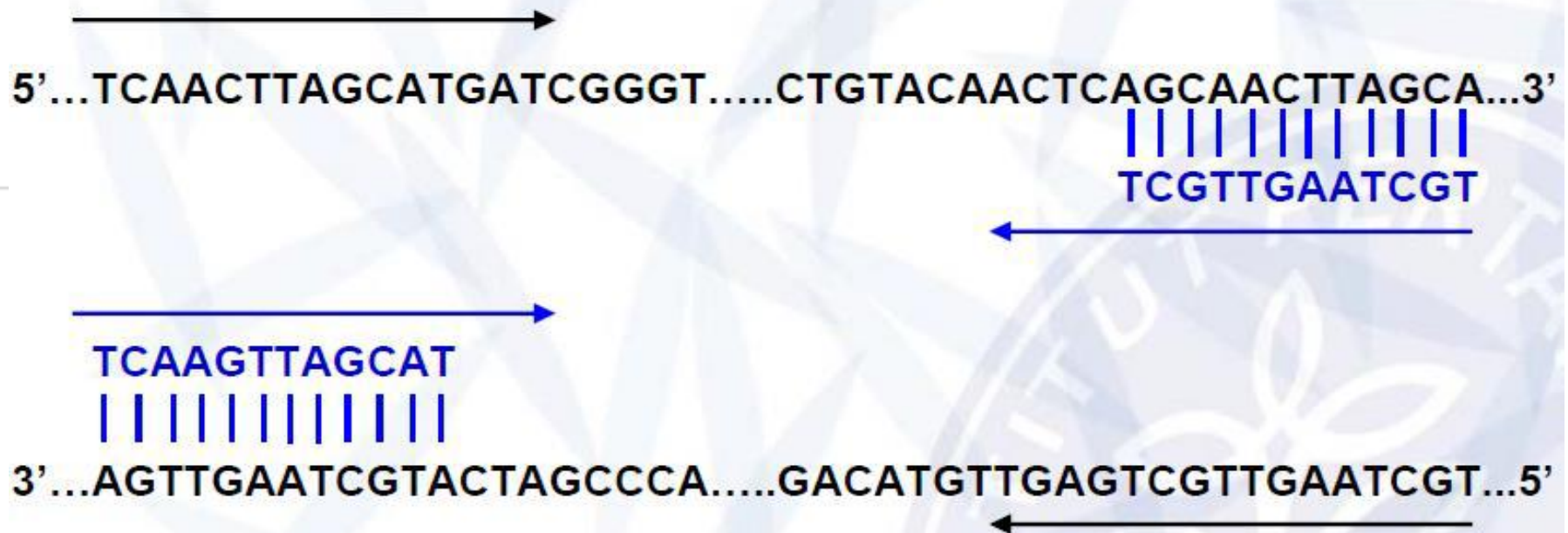
# DESAIN PRIMER

# Sasaran Perkuliahan

- Mahasiswa mampu menjelaskan tentang apa itu primer
- Mahasiswa Mampu menganalisis karakter primer yang baik
- Mahasiswa mampu mendesain urutan DNA primer sesuai dengan urutan gen yang diinginkan
- Mahasiswa mampu menghitung nilai  $T_m$  dan  $T_a$  primer



# DNA REPLICATION & PRIMER



Common primer is an oligonucleotide, a short segment of single-stranded DNA, used to replicate DNA from a fragment.

# Good Primers Characteristics

- Unique
- Has an appropriate melting- $(T_m)$  and annealing-temperature  $(T_a)$
- Random base distribution, and average G+C content ; Avoid long A+T and G+C-rich region if possible
- Usually 15-30 nucleotides in length
- Absence of dimerization capability
- Absence of significant hairpin formation

## Uniqueness

- There shall be only one target site in the template DNA where the primer binds
- The longer  $\rightarrow$  the more chance that it's unique
- The length  $\geq 15$  bases to ensure uniqueness

### Template DNA

5' .. TCAACTTAGCATGATCGGGTA .. GTAGCAGTTGACTGTACAACCTCAGCAACTTAGCA .. 3'

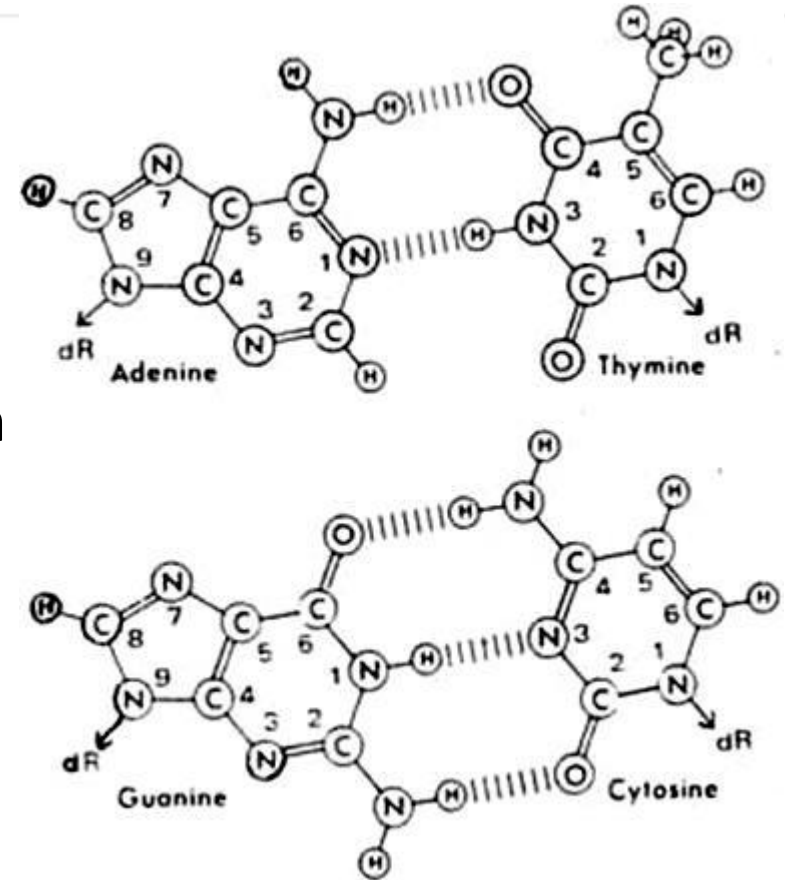
TGCTAAGTTG
CAGTCAACTGCTAC
TGCTAAGTTG

Primer candidate 1 5'-TGCTAAGTTG-3' **NOT UNIQUE!**

Primer candidate 2 5'-CAGTCAACTGCTAC-3' **UNIQUE!**

## Melting Temperature (T<sub>m</sub>)

- the temperature at which 50% of the DNA duplex dissociates to become single stranded
- Mostly determined by primer length and base composition
- Longer primer length and higher G/C content increase T<sub>m</sub>
- The optimal G/C content: 45-55%





## Melting Temperature (T<sub>m</sub>)

- Optimum T<sub>m</sub>: 52–65 °C, but higher T<sub>m</sub> is sometimes is recommended for high GC content targets.
- If a pair of primer is used to amplify a fragment, the T<sub>m</sub> difference between primer pair should be < 5 °C
- How to calculate T<sub>m</sub> Using an equation:
- Shorter than :  $T_m = 2(A+T) + 4(G+C)$
- T<sub>m</sub> Gabungan =  $(T_m \text{ forward} + T_m \text{ reverse})/2$
- Longer than :  $T_m = 64.9 + 41 * (G+C-16.4)/(A+T+G+C)$

# Melting Temperature ( $T_m$ ): how to calculate $T_m$

## Using softwares:

The screenshot shows the BioEdit Sequence Alignment Editor window with a ThermoCalc dialog box open. The ThermoCalc window is titled "ThermoCalc -- Tm calculation with mismatches". It contains the following fields and values:

- Na: 50 nM
- Mg: 0 mM
- Primer conc.: 250 nM (circled in red)
- Units: nM (selected), ug/ml
- Seq 1: CGGAGGCGAAGGCGGCGAAG
- Seq 2: CGGAGGCGAAGGCGGCGAAG
- Length: 20
- delta H: -167.40 Kcal/mol
- delta S: -462.15 eu
- delta S (standard -- 1M NaCl): -441.20 eu
- delta G: 37 cal/mol-24.05 Kcal/mol
- delta G, 37 S (standard -- 1M NaCl): -30.54 Kcal/mol
- Primer 1 G+C: 75.00%
- Primer 2 G+C: 75.00%
- Tm: 64.96-C

Buttons at the bottom include "Calculate", "Close", and "Parameters -->".

**We must know the additional information by ourselves**

## 2. Untuk melihat GC content dan TM pada program online “Oligo Calc”

The screenshot shows the Oligo Calc: Oligonucleotide Properties Calculator interface. The user has entered the sequence TCA CGG CCA GCC TTG CTC CAC CTT. The reverse complement strand is shown as AAG GTG GAG CAA GGC TGG CCG TGA. The calculated properties are as follows:

Physical Constants		Melting Temperature (T <sub>M</sub> ) Calculations	
Length:	24	Molecular Weight:	7200.74
GC content:	63 %	1	62.5 °C (Basic)
1 ml of a sol'n with an Absorbance of		2	NaN °C (Salt Adjusted)
is	0 microMolar	3	NaN °C (Nearest Neighbor)
and contains			
<b>Thermodynamic Constants Conditions: 1 M NaCl at 25°C at pH 7.</b>			
RlnK	NaN cal/(°K* <sup>2</sup> mol)	deltaH	209.4 Kcal/mol
deltaG	36.4 Kcal/mol	deltaS	541.6 cal/(°K* <sup>2</sup> mol)

# Annealing Temperature ( $T_a$ )

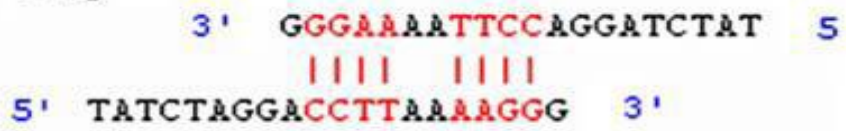
- $T_a$  is the temperature at which primers anneal to the template DNA.
- $T_a$  can be calculated from  $T_m$ .
- General rule:  $T_a$  is 5°C lower than  $T_m$  ( $T_a = T_m - 5^\circ\text{C}$ )  
$$\text{Suhu Annealing} = T_m \text{ Gabungan} - 5^\circ\text{C}$$
- Higher  $T_a$  enhances specific amplification but may lower yields

# Primer Dimer

- Primer molecules that have attached (hybridized) to each other because of strings of complementary bases in the primers.
- Primer dimer could decrease the PCR efficiency dramatically.

## Self-Dimer

8 bp



4 bp



## Dimer

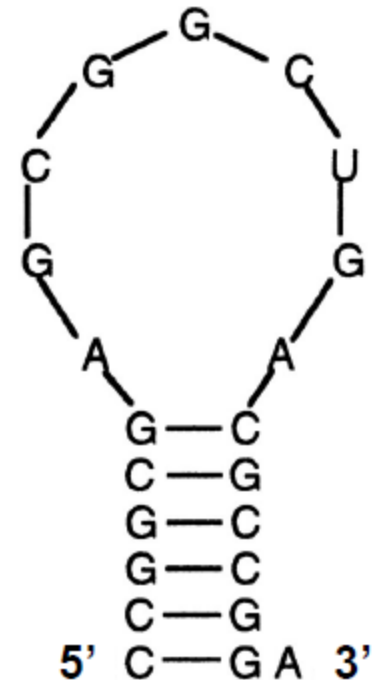
forward primer



reverse primer

# Hairpin Formation

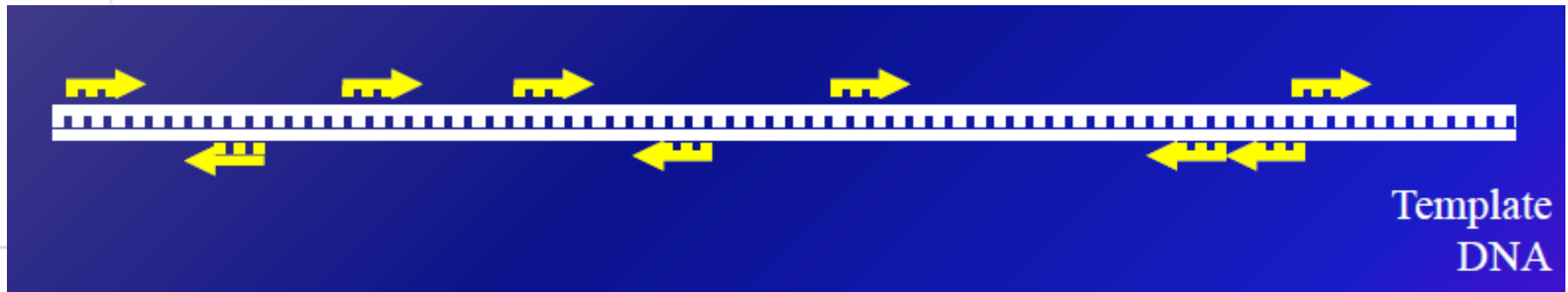
- Occurs when two regions of the same strand of the primer base-pair resulting lollipop-shaped structure
- Hairpin formation will lead unfunctional primer and could decrease the PCR efficiency dramatically.
- Sometimes primer dimer and hairpins are harmless when the annealing temperature does not allow them to take form. (i.e. some dimers or hairpins form at 30 °C while during PCR cycle, the lowest temperature only drops to 60 °C).



# Application of Primers

- Molecular Marker (RAPD, SSR, ISSR, etc.)
- Gene cloning *gene specific primer, degenerate primer, adapter primer*
- PCR-based gene expression studies *PCR, Real-time PCR*
- Constructing probes *Northern-, Southern-blot, Micro-array*
- Sequencing

# RAPD Primers



- Only 1 primer per reaction
- Uses 10 base primers for PCR
- Primer binds to many locations on the template DNA
- Only when primer binding sites are close and oriented in opposite directions so the primers point toward each other will amplification take place



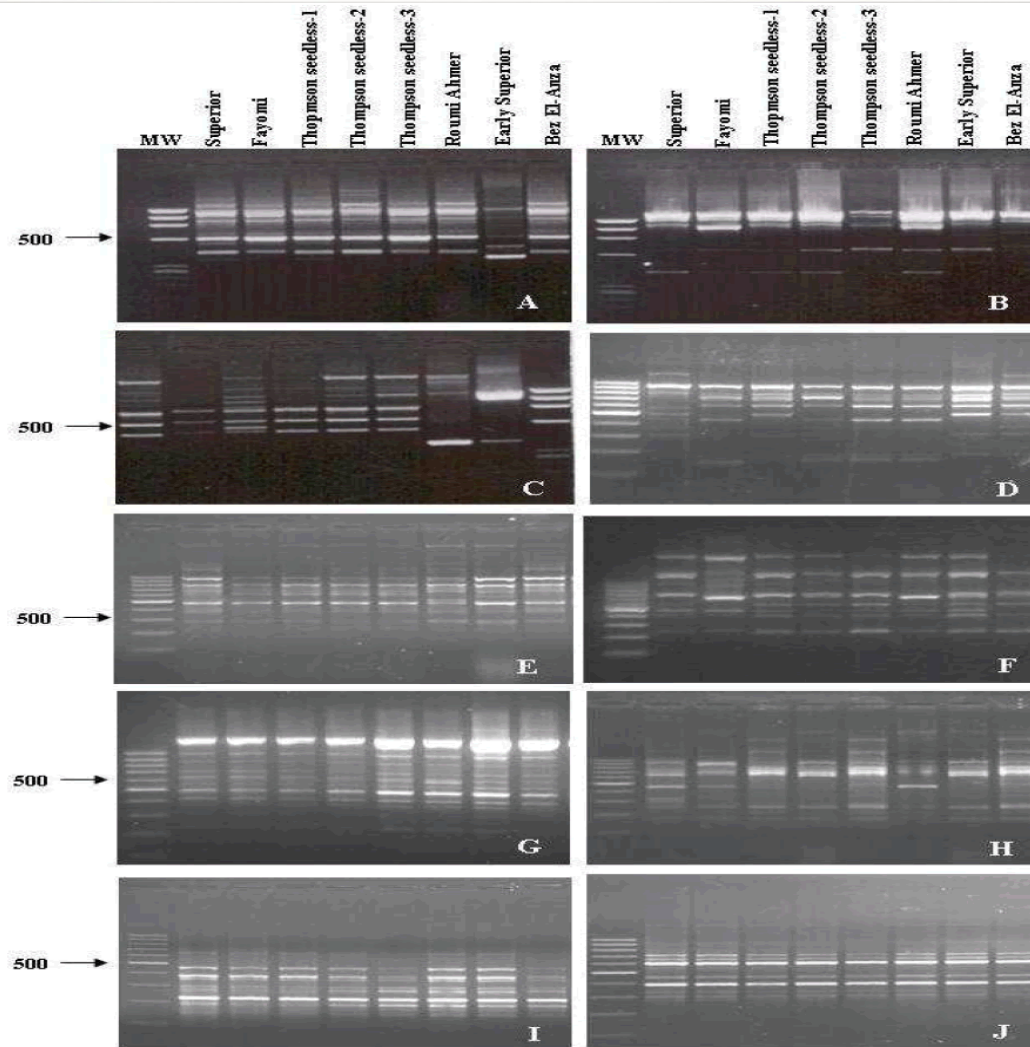
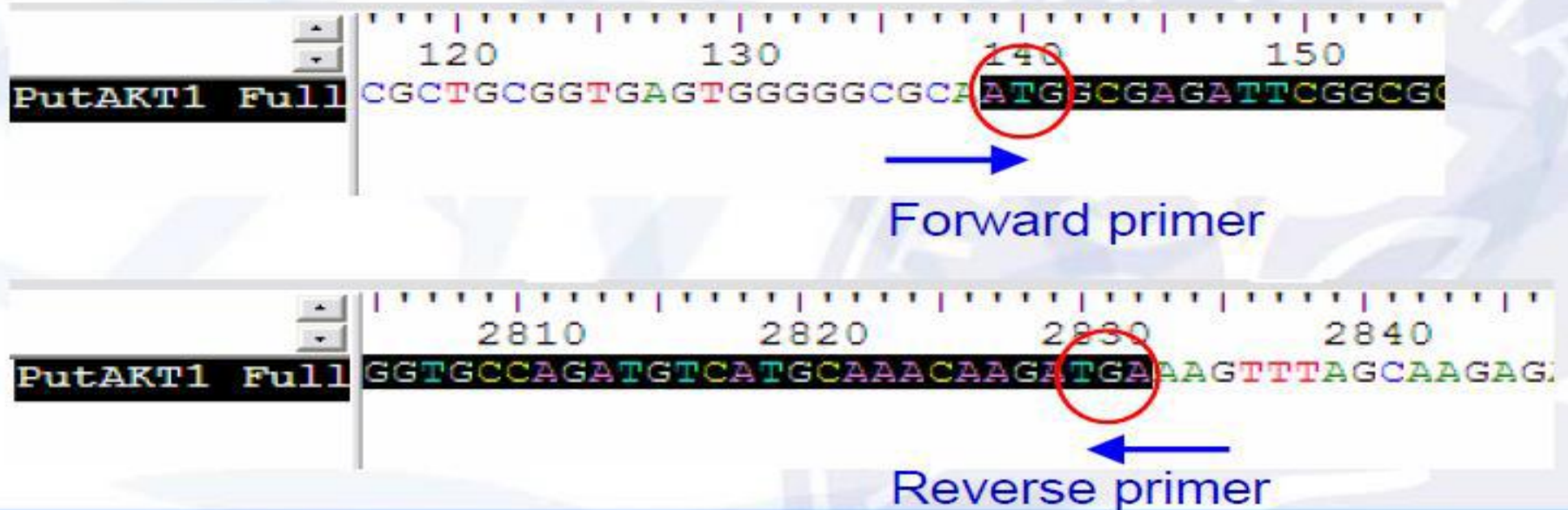


Figure 2: RAPD fingerprinting of 8 local Egyptian grape cultivars (*Vitis vinifera* L.). (A)Primer OP-A03; (B)Primer OP-A07; (C) Primer OP-A11; (D)Primer OP-A15; (E) Primer OP-B02; (F)Primer OP-B07; (G)Primer OP-B16 ; (H)Primer OP-B19; (I)Primer OP-G19 and (J)Primer OP-G20

# Primers Design in Gene Cloning

- Primers work in pairs –forward primer and reverse primer.
- location of the primer on the template DNA should consider the start-and stop-codon.



# Degenerate Primers

- Untuk identifikasi anggota baru / gen dari gen yang sama pada individu yang berbeda
- Berasal dari percampuran/ sequen yang sama
- Mengandung perbedaan urutan nekleotida pada lokasi tertentu
-

# Degenerate Primers

- Digunakan secara bersamaan dengan harapan salah satu urutan DNA akan melengkapi gen target
- Urutan asam amino dari protein yang dikenal
- Primer yang dibentuk untuk mendapatkan sekuen DNA yang belum diketahui diambil dari urutan asam amino protein yang dikenal

AspGluGlyPheLeuSerTyrCysTrpLeuProHisGln  
 GATGAAGGTTTCTTTCTTATTGTTGGCTTCCATCAA  
 C G C CT CAGC C C T C C C G  
 A A A A A  
 G G G G G

A total of 32 unique oligonucleotides  
 would be generated

TATTGTTGGCTTCC  
 TACTGTTGGTCCC  
 TATTGCTGGCTTCC  
 TACTGCTGGCTTCC  
 etc.

TAYTGYTGGYTNC

## Standard MixBase Definitions

R	A, G
Y	C, T
M	A, C
K	G, T
S	C, G
W	A, T
H	A, C, T
B	C, G, T
V	A, C, G
D	A, G, T
N	A, C, G, T

Amino Acid	3-Letter Code	1-Letter Code
Alanine	Ala	A
Cysteine	Cys	C
Aspartic acid or aspartate	Asp	D
Glutamic acid or glutamate	Glu	E
Phenylalanine	Phe	F
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Lysine	Lys	K
Leucine	Leu	L
Methionine	Met	M
Asparagine	Asn	N
Proline	Pro	P
Glutamine	Gln	Q
Arginine	Arg	R
Serine	Ser	S
Threonine	Thr	T
Valine	Val	V
Tryptophan	Trp	W
Tyrosine	Tyr	Y

### Universal Genetic Code Chart

Messenger RNA Codons and Amino Acids for Which They Code

		Second base				
		U	C	A	G	
First base	U	UUU } PHE UUC } UUA } LEU UUG }	UCU } UCC } SER UCA } UCG }	UAU } TYR UAC } UAA } STOP UAG }	UGU } CYS UGC } UGA } STOP UGG } TRP	U C A G
	C	CUU } CUC } LEU CUA } CUG }	CCU } CCC } PRO CCA } CCG }	CAU } HIS CAC } CAA } GLN CAG }	CGU } CGC } ARG CGA } CGG }	U C A G
	A	AUU } AUC } ILE AUA } AUG } MET or START	ACU } ACC } THR ACA } ACG }	AAU } ASN AAC } AAA } LYS AAG }	AGU } SER AGC } AGA } ARG AGG }	U C A G
	G	GUU } GUC } VAL GUA } GUG }	GCU } GCC } ALA GCA } GCG }	GAU } ASP GAC } GAA } GLU GAG }	GGU } GGC } GLY GGA } GGG }	U C A G

# UNiversal Primers

Primers can be designed to amplify only one product.  
Primers can also be designed to amplify multiple products (“universal primers”).

Strategy:

1. Align groups of sequences you want to amplify.
2. Find the most conservative regions at 5' end and at 3' end.
3. Design forward primer at the 5' conservative region.
4. Design reverse primer at the 3' conservative regions.
5. Matching forward and reverse primers to find the best pair.
6. Ensure uniqueness in all template sequences.
7. Ensure uniqueness in possible contaminant sources



## Computer – aided primer design

Some primer design programs we use:

**-Oligo:Life Science Software, standalone application**

**-GCG: Accelrys, ICBR maintains the server.**

**-Primer3:MIT, standalone / web application**

[http://www-genome.wi.mit.edu/cgi-bin/primer/primer3\\_www.cgi](http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi)

**-BioTools:BioTools, Inc. ICBR distributes the license.**

**-Others:GeneFisher, Primer!, Web Primer, NBI oligo program, etc.**

Melting temperature calculation software:

**-BioMath: <http://www.promega.com/biomath/calc11.htm>**

## TUGAS PRAKTIKUM ---- KUMPULKAN MINGGU DEPAN

1. Buatlah Desain primer dari suatu gen tertentu atau dari spesies tertentu. lakukan analisis primer tersebut secara online dan secara manual, Nilai **T<sub>m</sub>** masing – masing primer dan nilai **T<sub>a</sub>** nya
2. bandingkan hasil keduanya dan analisis kelebihan dan kekurangannya

THANK  
YOU



607132.wordpress.com

Noviani's Blog

