## 'Glass Half Full or Empty': Illuminating the Human Transcriptome

Lecture 2

### Any questions from last class?

# Worksheet Answers! (from last class)

#### Let's review some big themes!

- 1) Central dogma of biology
- 2) DNA has two strands that pair with each other
  - 3) Alternative splicing

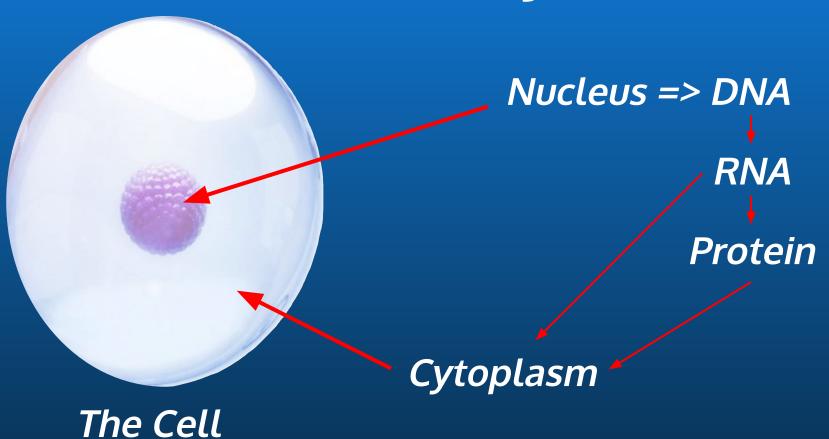
## The World of Biology



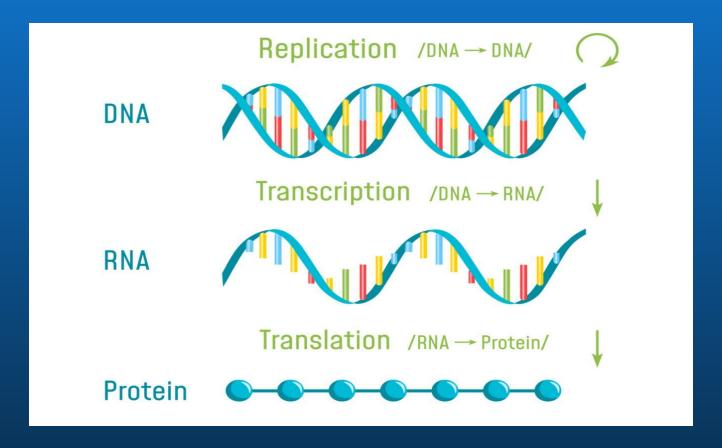


The Cell

#### The Central Dogma



#### The Central Dogma



## The Central Dogma

DNA

RNA

**Protein** 







Eggs

Beef

Cheese

Bacon

Lettuce

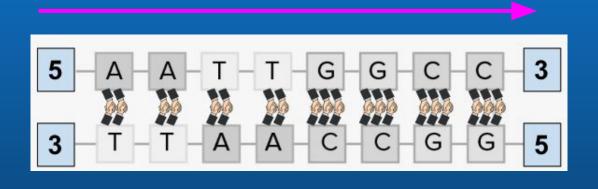
**Pickles** 

**Tomato** 

**Bread** 

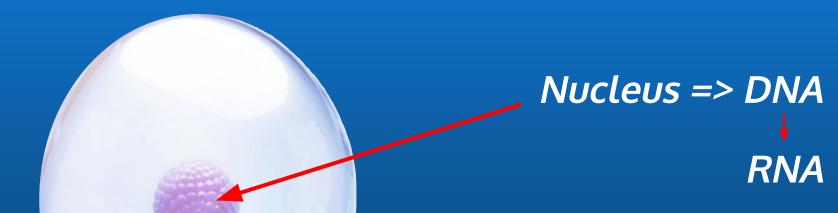
Mayo

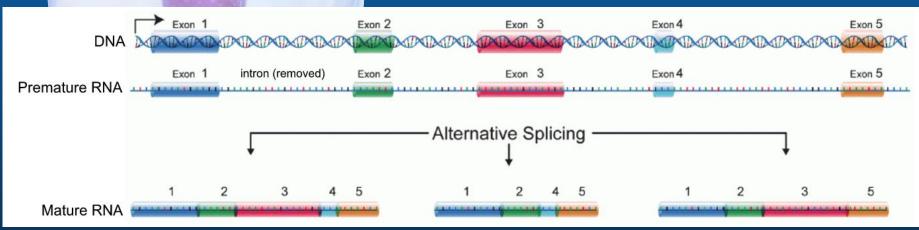
#### DNA has two strands that base pair with each other



NOTICE: The 5' end of one strand pairs with the 3' end of the other!

#### Alternative splicing





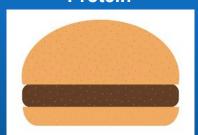
### **Alternative splicing**

**DNA** 

**RNA** 



**Protein** 







Eggs
Beef
Cheese
Bacon
Lettuce
Pickles
Tomato
Bread
Mayo

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So... what's next?

You are working on a NOVEL research project!

So.... what's the research question?



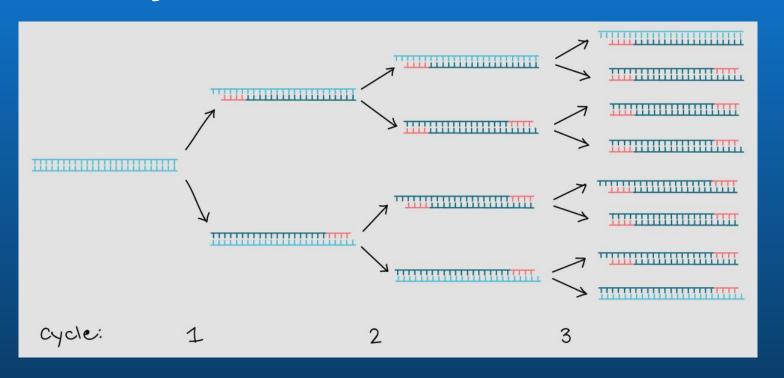
Can we predict <u>NEW</u> transcripts (mature RNA) and prove that they exist?

#### Yes!!!

- 1) Predict new transcripts (RNA)
- 2) Harvest transcripts (as stable DNA) from cells
  - 3) Amplify your transcript
    - 4) Isolate your transcript
  - 5) <u>Sequence</u> the transcript

#### Yes!!!

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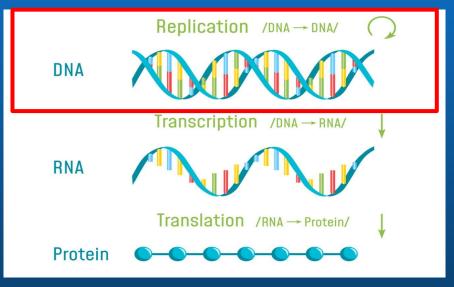


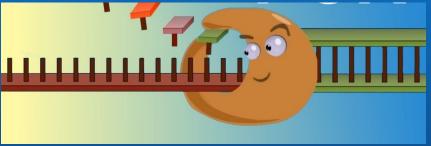
#### Where have you heard this term...





... is inspired by DNA replication!

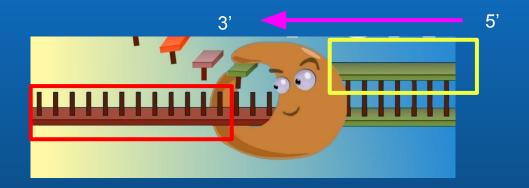


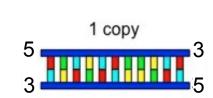


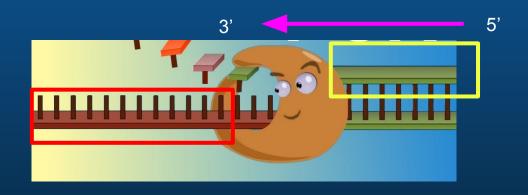
**DNA polymerase** 'the **DNA builder**'

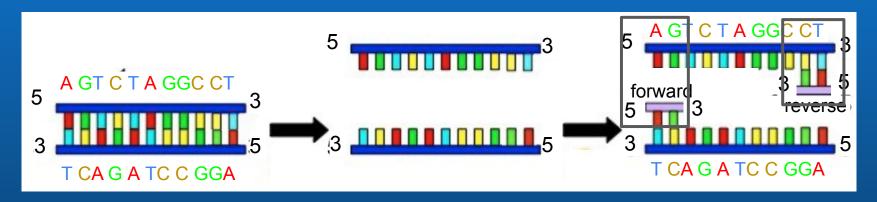
#### **DNA polymerase** needs 3 things

- Template DNA (red)
- 2. **Primer** (yellow) = 'an anchor'
- 3. New bases







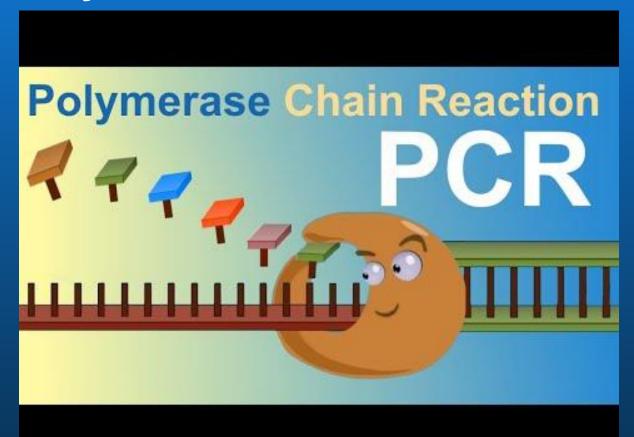


What's the sequence of the 2-base forward primer? 5'-AG-3' same as top strand

What's the sequence of the 2-base reverse primer? 5'-AG-3'

'reverse complement' of top strand 5'-CT-3'

Answer by writing it in the 5' -> 3' orientation.



#### **Worksheet Time!**

## Time to select some transcripts & design some primers!

#### After designing primers go to...

https://www.bioinformatics.org/sms2/pcr\_primer\_stats.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 Manipulation Suite:

#### **PCR Primer Stats**

PCR Primer Stats accepts a list of PCR primer sequences and returns a report describing the properties of each primer, including melting temperature, percent GC content, and PCR suitability. Use PCR Primer Stats to evaluate potential PCR primers.

Paste the raw sequence or one or more FASTA sequences into the text area below. Input limit is 5,000,000 characters. The maximum accepted primer length is 50 bases.

>reverse

aacagctatgaccatg

>forward

agtcgatcgatgagaa

Submit

Clear

Reset