



SENIOR BIOLOGY

Blueprint of life and Genetics: the Code Broken?

NAME

SCHOOL / ORGANISATION

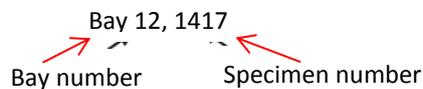
DATE

INSTRUCTIONS

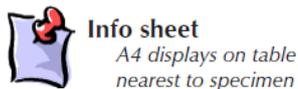
1. Make sure you read the bold text in boxes throughout the worksheet as they contain important information

These boxes contain instructions explaining how to complete the next section of your worksheet

2. To find a particular disease or specimen you may need to refer to its specimen number. Once you have found the bay, the specimen will have a purple label to help you locate it on the shelf.



3. Detailed information about a specific disease or specimen will either be found on an info sheet, poster or next to the specimen itself. The following symbols are used throughout the worksheet.



Info sheet
A4 displays on table nearest to specimen



Poster
located throughout museum



Observation
Find exhibit and describe features

IMPORTANT

Real people have generously donated their body so that medical scientists can learn about health and disease. Our donors deserve the utmost respect and admiration for their invaluable contribution to medical science.

INTRODUCTORY NOTES



Blueprint of Life

In this part of the workshop you will address the following syllabus points;

Activity: Punnett Square – Online Punnett square tutorial

- distinguish between homozygous and heterozygous genotypes in monohybrid crosses
- perform an investigation to construct pedigrees or family trees, trace the inheritance of selected characteristics and discuss their current use
- distinguish between the terms allele and gene, using examples
- explain the relationship between dominant and recessive alleles and phenotype using examples
- solve problems involving monohybrid crosses using Punnett squares

Activity: Blood type – online module

- compare the inheritance of the ABO and Rhesus blood groups
- solve problems to predict the inheritance patterns of ABO blood groups

Genetics: The Code Broken?

In this part of the workshop you will address the following syllabus points;

Activity: BLAST

- distinguish between mutations of chromosomes, including;
 - rearrangements
 - changes in chromosome number, including trisomy, and polyploidy
- and mutations of genes, including;
 - base substitution
 - frameshift

Activity: BLAST

- process and analyse information from secondary sources to describe the effect of one named and described genetic mutation on human health
- process information from secondary data to outline the current understanding of gene expression

Activity Station 1: Punnett Square – Online Punnett square tutorial – iPad task

[Punnett squares:](http://bit.ly/mohdpunnettute) <http://bit.ly/mohdpunnettute>

Activity Station 2: Effect of Environment on cell Genotype – Skin Bay Specimens (Bay 12)

Compare specimens 903 and 2995, and the details about them in the catalogues.

Activity Station 3: Blood type – online module

compare the inheritance patterns of Codominance instances

[Genetics tutorial:](http://bit.ly/mohdbiogentute) <http://bit.ly/mohdbiogentute>

Activity Station 4: BLAST 1 – Computer Lab

Introduction

Today you are a medical research scientist in a pathology lab who has sequenced part of a patient's DNA. You are not sure what the DNA codes for, but you have 100 nucleotide base pairs of the DNA.

To find out what gene your nucleotide sequence codes for, you will be running an internet-based BLAST search. BLAST, or the Basic Local Alignment Search Tool, compares your sequence with a very large database of known DNA sequences that scientists around the world have compiled.

Find out what your mystery sequence encodes using a BLAST search:

1. Go to the BLAST website: <http://blast.ncbi.nlm.nih.gov/Blast.cgi>
2. Select “nucleotide” button.
3. Copy and paste the whole of one of the CFTR mystery sequences below into the “Enter accession number” box at the top of the page. **(Figure 1 at end of worksheet)**

>Mystery sequence 1 (in-frame del)

```
GAATTTCACTTCTGTTCTCAGTTTTCTGGATTATGCCTGGCACCATTAAAGAAAATATCATCGGTGTTTCCTATGATGAAT
ATAGATACAGAAGCGTCA
```

>Mystery sequence 2 (frameshift del)

```
TGGACCAGACCAATTTTGAGGAAAGATACAGACAGCGCCTGGAATTGTCAGACATATACCAAATCCCTTCTGTTGATTC
TGCTGACAATCTATCTGAA
```

>Mystery sequence 3 (frameshift substitution)

```
TGTGTCTGTAAACTGATGGCTAACAAAAGTAGGATTTGGTCACTTCTAAAATGGGACATTTAAAGAAAGCTGACAAAA
TATTAATTTTGCATGAAGGTAGC
```

>Mystery sequence 4 (synonymous mutation)

```
GACTTCATCCAGTTGTTATTAATTGTGATTGGGGCTATAGCAGTTGTCGCAGTTTTACAACCCTACATCTTTGTTGCAACA
GTGCCAGTGATAGTGGCTTTT
```

4. Under “Choose Search Set” select “Human Genomic + transcript” **(Figure 1 at end of worksheet)**
5. Hit the “BLAST” button at the bottom of the page.. **(Figure 1 at end of worksheet)**
6. Once your BLAST report comes up on the screen, scroll down to the “Alignments” heading. There will be a series of matching sequences that the search found on the database. **(Figure 2 at end of worksheet)**
7. In the top sequence identify the difference and circle it in the sequence above.
8. How many base pairs in the whole gene? _____
9. Which pairs does this short sequence correspond to on the whole gene? _____

10. Repeat for the other sequences then complete the following.



11. Write down the name of the gene your sequence matches. You'll find the name of the gene in the alignment data.

12. Click on the "genbank" link at the top of the description. **(Figure 2 at end of worksheet)**

13. Scroll down and on the right hand side of the page click on "More about gene"

As a pathologist, you need to understand what this gene does in the body.

a) On what chromosome is this gene found? _____

b) What is the function of the protein coded by this gene?

c) What disorders are associated with defective versions of this protein?

The CFTR gene is just one of many on human chromosome 7. Use the chromosome viewer in the banner in the top right hand of the screen to look at how many disorders are caused by genes on chromosome 7.

(Figure 3 at end of worksheet)

http://web.ornl.gov/sci/techresources/Human_Genome/posters/chromosome/index.shtml

14. Use this information to answer the following questions:

g) How many base pairs make up this chromosome? Compare the number of base pairs on chromosomes 1, 7 and 21. _____

h) Browse through the various disorders associated with genes on this chromosome. Name five different parts of the body that could be affected by mutations on this chromosome?

Scientists have found more than 1000 different mutations of the CFTR gene; Some have little or no effect on CFTR function, while others cause cystic fibrosis on a spectrum that varies from mild to severe. Click on this link to view a database of all known mutations in the CFTR gene.

<http://www.genet.sickkids.on.ca/cftr/Home.html>

The mutations present in your mystery sequences are by far the most common mutation observed in cystic fibrosis patients. The deletion of three base pairs in the CFTR gene causes the loss of an amino acid called phenylalanine at position 508 and the protein does not fold correctly.

Normal CFTR proteins, once translated and synthesised, are transported to the endoplasmic reticulum (ER) and golgi apparatus before they are integrated into the cell membrane. Incorrectly folded CFTR proteins are recognised by the ER and are destroyed before they reach the cell membrane.

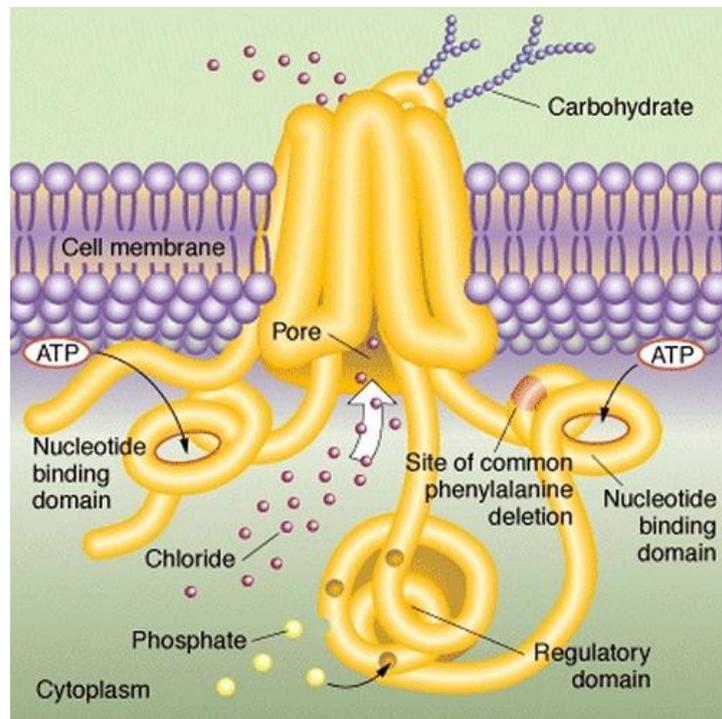


Diagram of how the CFTR protein forms a channel for chloride ions through the membrane of a cell. Image credit: <http://massgenomics.org/2011/02/a-promising-new-drug-for-cystic-fibrosis.html>

Activity Station 6: Virtual Microscopy

Go to the Microscopy room G05B

Open the link to the annotated CF slide:

[https://www.best.edu.au/s/j5ne1cw5/xbfsetze?data=7%40\[\]!8%40!9%409408!10%40-4986&version=1](https://www.best.edu.au/s/j5ne1cw5/xbfsetze?data=7%40[]!8%40!9%409408!10%40-4986&version=1)

What organ is this slide from?

In this slide the stain makes; fibre (scar) Pink, DNA purple and leaves water/air/fat clear.

Using the annotations and zoom function label significant areas on this slide.

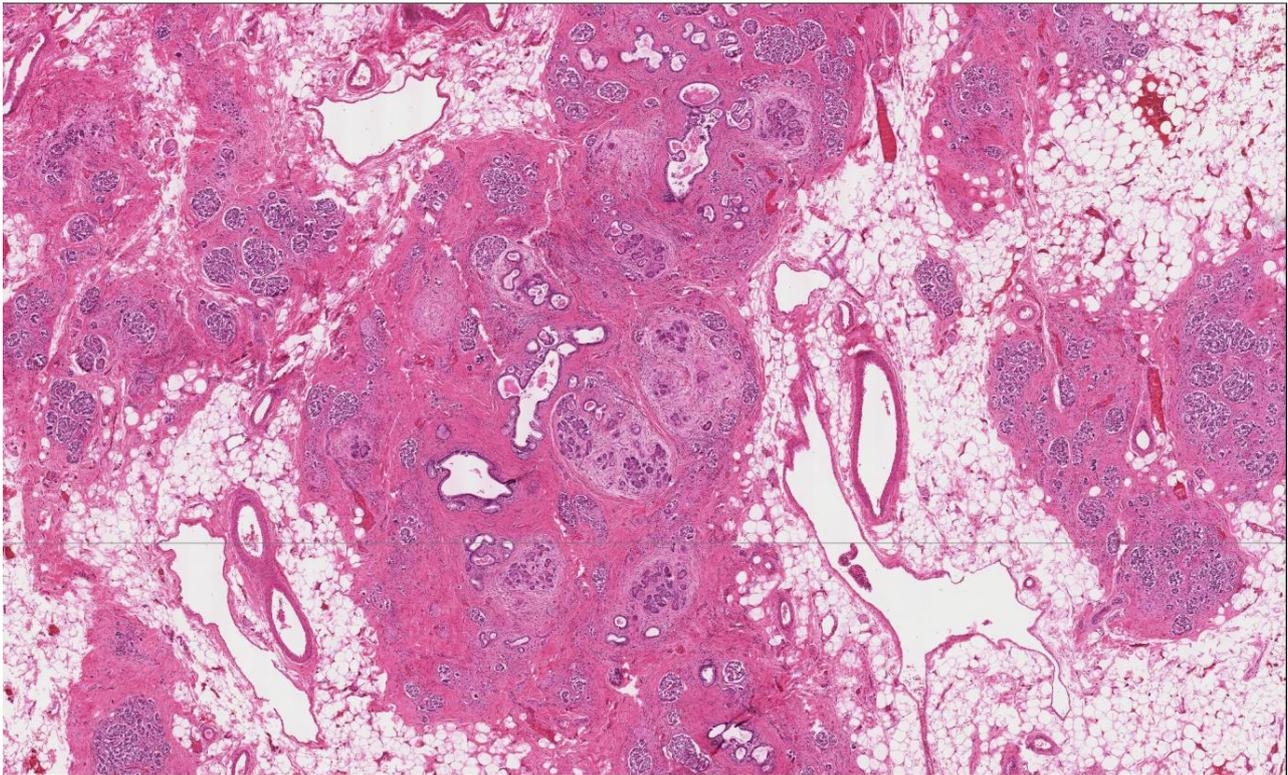


Figure 1 BLAST screen 1

BLAST® » blastn suite

Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

BLASTN programs search nucleotide databases using a nucleotide query sequence.

Step 3 Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear] Query subrange [From:] [To:]

Or, upload file [Browse...] No file selected.

Job Title [Enter a descriptive title]

Align two or more sequences

Step 4 Choose Search Set

Database: Human genomic + transcript Mouse genomic + transcript Others (nr etc.):

Human genomic plus transcript (Human G+T) (176974 sequences)

Exclude: Models (XM/XP) Uncultured/environmental sample sequences

Limit to: Sequences from type material

Entrez Query: [Enter an Entrez query to limit search] [YouTube](#) [Create custom database](#)

Program Selection

Optimize for: Highly similar sequences (megablast) More dissimilar sequences (discontiguous megablast) Somewhat similar sequences (blastn)

Choose a BLAST algorithm

Step 5 BLAST [Sequences] using Megablast (Optimize for highly similar sequences)

Figure 2 BLAST screen

Sequence logo for alignments scores

Query: 1 20 40 60 80 100

Descriptions

Sequences producing significant alignments:

Select: All None Selected: 0

Alignments [Download] [GenBank] [Graphics] [Distance tree of results]

Description Transcripts

PREDICTED: Homo sapiens cystic fibrosis transmembrane conductance regulator (CFTR), transcript variant X4, mRNA

PREDICTED: Homo sapiens cystic fibrosis transmembrane conductance regulator (CFTR), transcript variant X3, mRNA

PREDICTED: Homo sapiens cystic fibrosis transmembrane conductance regulator (CFTR), transcript variant X1, mRNA

PREDICTED: Homo sapiens cystic fibrosis transmembrane conductance regulator (CFTR), transcript variant X2, mRNA

Homo sapiens cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7) (CFTR), mRNA

Genomic sequences [show first]

Homo sapiens chromosome 7, alternate assembly CHM1.1.1

Homo sapiens chromosome 7, GRCh38.p7 Primary Assembly

Alignments

[Download] [GenBank] [Graphics]

PREDICTED: Homo sapiens cystic fibrosis transmembrane conductance regulator (CFTR), transcript variant X4, mRNA

Sequence ID: XM_011515754.2 Length: 7

Range 1: 2965 to 3066 [GenBank] [Graphics]

| Score | Expect | Identities | Gaps | Strand |
|--------------|--------|--------------|-----------|-----------|
| 183 bits(99) | 2e-44 | 101/102(99%) | 0/102(0%) | Plus/Plus |

Query 1 TGTGTCTGTAAACTGATGGCTAACAAAACCTAGGATTTGGTCACTTCTAAATGGGACAT 60

Sbjct 2965 TGTGTCTGTAAACTGATGGCTAACAAAACCTAGGATTTGGTCACTTCTAAATGGGACAT 3024

Query 61 TTAAGAAAAGCTGCACAAAATATTAAATTTGGCATGAAAGTATGC 102

Sbjct 3025 TTAAGAAAAGCTGCACAAAATATTAAATTTGGCATGAAAGTATGC 3066

Step 6 (pointing to Descriptions)

Step 12 (pointing to Alignments)

Figure 3 GENE poster screen

Human Genome Project 1990-2003 **Step 14** Archive

About the HGP | Research | Publications | Site Map | Contact Us

Archive Site Provided for Historical Purposes

Gene Gateway - Exploring Genes and Genetics Disorders

A Web Companion to the Human Genome Landmarks Poster

home | workbook

chromosome viewer 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

Chromosome 7

The chromosome image below is the online version of chromosome 7 depicted on the Human Genome Landmarks poster.

Mouse over image to zoom

150 million base pairs

Human Genome Landmarks

Human Genome Landmarks: Selected Genes, Traits, and Disorders - Download PDF Each of the 24 different human chromosomes featured on this poster can be viewed online.

Human Genome Project 1990-2003

The Human Genome Project (HGP) was an international 13-year effort, 1990 to 2003. Primary goals were to discover the complete set of human genes and make them accessible for further biological study, and determine the complete sequence of DNA bases in the human genome. See [Timeline](#) for more HGP history.

Human Genome News

Published from 1989 until 2002, this newsletter facilitated HGP communication, helped prevent duplication of research effort, and informed persons interested in genome research.

[Click Here for Printable Image](#)
Visit the [Image Gallery](#) for high-resolution print-quality version.

Legend: