**Start Here**

Search for REU site keywords: proteomics, genomics, computational biology, genetics, bioinformatics, transcriptomics, and biochemistry

<https://www.nsf.gov/crssprgm/reu/reu_search.jsp>

Platforms

NCBI Pubmed <https://pubmed.ncbi.nlm.nih.gov/>

NCBI Gene <https://www.ncbi.nlm.nih.gov/gene/>

NCBI Protein <https://www.ncbi.nlm.nih.gov/protein/>

SWISS-Model Expasy <https://swissmodel.expasy.org/>

Mind the Graph (allows 1 free image to be created) <https://mindthegraph.com/>

Teaching and learning multiomics into lecture can build alignment with research skills and REUs to apply to. Many courses ask students to write a paper on a condition or disease topic. Here we extend the paper to add digital experiences to extend the paper to understanding how the central dogma is applied in the disease topic of interest with hands on digital applications and platforms commonly used in laboratory research. Instructors may related the module to humans or other living organisms.

**Learning objectives**

To acquire data acquisition and visualization skills from genomics, transcriptomics and proteomics for CV or resume additions.

Synthesize of the interplay between genes, RNA, and proteins using digital platforms in lecture to see the process of science.

Genetic mutations will be identified to molecular and physiological processes.

Data mining and analysis will be used to build research skills and a graphical abstract will be used to build scientific communication skills useful in REUs.

These research and communication skills may be used to build the CV for undergraduates and support application submissions to REUs.

**Length of Time**

2 hours total including instruction and questions. Spread over 4 class sessions or 1-2 long sessions.

Class one- Identify clinical condition, implicated gene, and genetic anomaly.

Class two-Determine RNA-seq expression

Class three-Extract protein sequence and create a protein model

Class four- Communicate science with a graphical abstract. Add new skills to the CV or resume

**Research skills that can be added to the CV or Resume applicable to REU applications**

**Literature review** of clinical conditions with PubMed and identification of genes with anomalies that lead to clinical conditions  
**RNA sequence acquisition** with data mining in NCBI Gene. Analysis of expression to determine if expression aligns with clinical condition  
**Protein sequence and structure acquisition** using NCBI protein and Expasy Swiss Pro to determine protein structure and critical potential residues for further targeting  
Communication of results with **creating a graphical abstract** using Mind the Graph

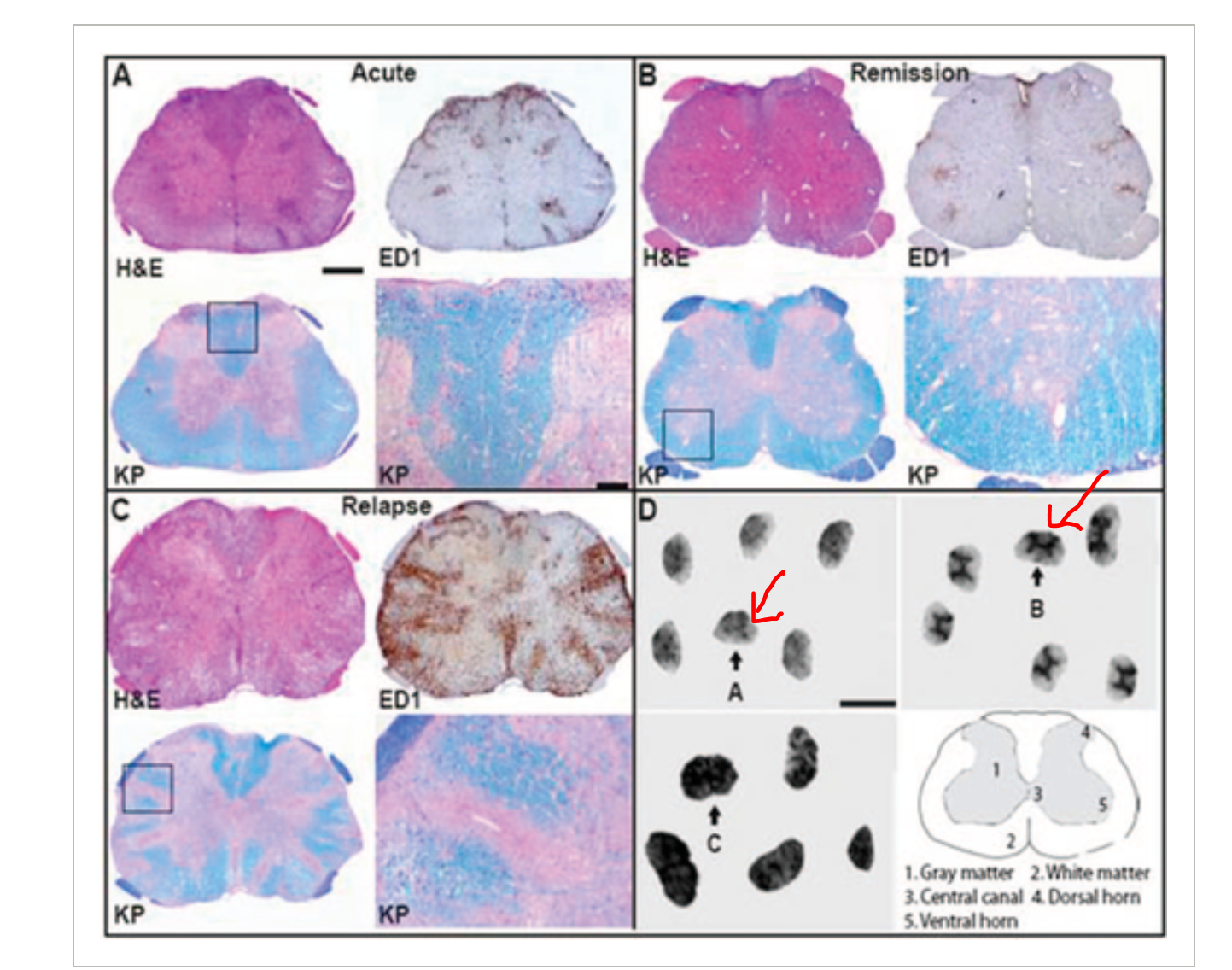
**Potential Resulting Examples**

**Identify a condition of interest and an associated contributing gene using Pubmed. Describe the condition in the introduction of your report. Describe the gene name and genetic anomaly.**

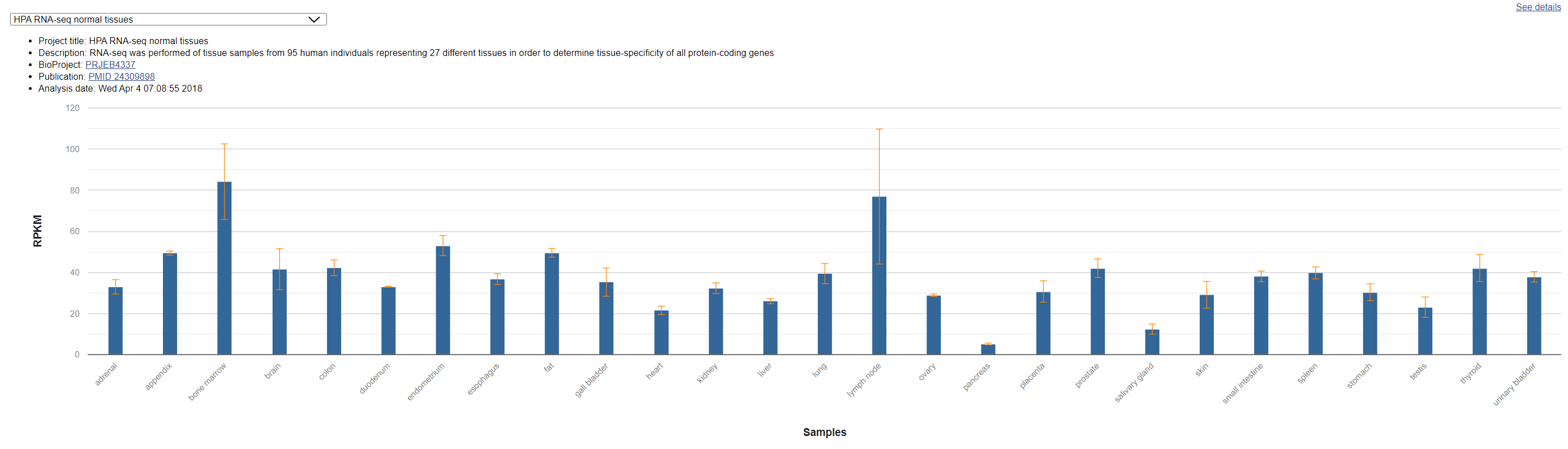
[**https://pubmed.ncbi.nlm.nih.gov/31728855/**](https://pubmed.ncbi.nlm.nih.gov/31728855/)

Multiple sclerosis in humans, HMGB1 overexpression

**Figure 1.**



Use Pubmed Gene to look up the associated gene. In NCBI Gene- add the gene name- and SEARCH. Select human. Scroll down to see the RNA-Seq expression data. Capture the date in your report. Label as **Figure 2 and create a figure legend.**



Note to instructors- the gene is up the student or instructors. As instructor you may select a specific condition and specific gene so students work on 1 gene or let everyone find a gene of their interest and each person will have a unique research experience.

**Figure 3a. Extract the FASTA sequence from NCBI pubmed of the described protein of the gene**

[**https://www.ncbi.nlm.nih.gov/protein/CAG33144.1?report=fasta**](https://www.ncbi.nlm.nih.gov/protein/CAG33144.1?report=fasta)

# HMGB1 [Homo sapiens]

GenBank: CAG33144.1

[GenPept](https://www.ncbi.nlm.nih.gov/protein/CAG33144.1?report=genpept) [Identical Proteins](https://www.ncbi.nlm.nih.gov/ipg/CAG33144.1) [Graphics](https://www.ncbi.nlm.nih.gov/protein/CAG33144.1?report=graph)

>CAG33144.1 HMGB1 [Homo sapiens]

MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKAR

YEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADD

KQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSKKKKEEEEDEEDEEDEEEEEDEEDEDEEE

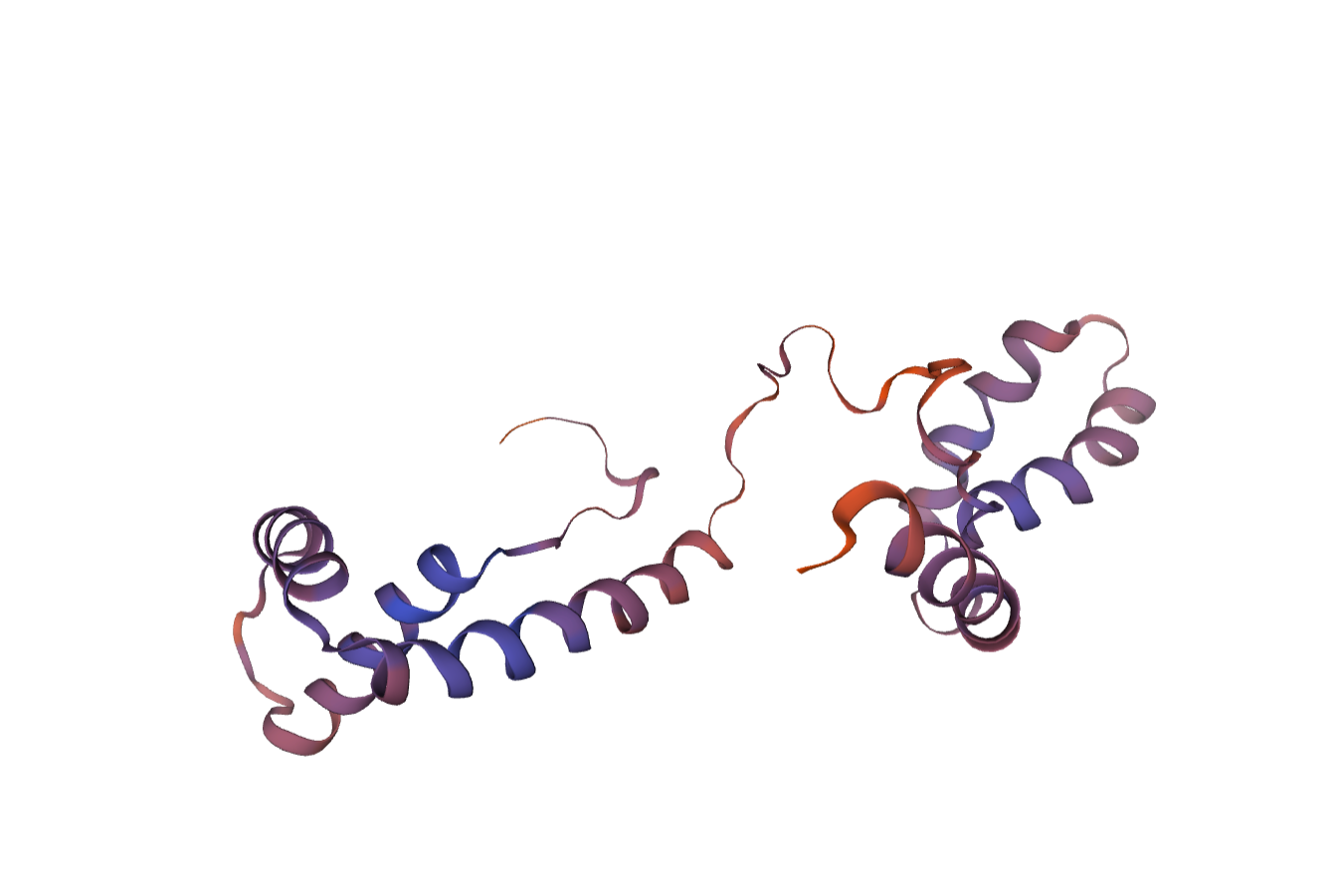
DDDDD

Instructors may ask questions about the protein sequence:

What is the amino acid aligned with the start codon?  
What is the accession number?  
How many amino acids are there?

Build a model of the protein. Use the FASTA sequence to create a protein model in Swiss-Model Expasy

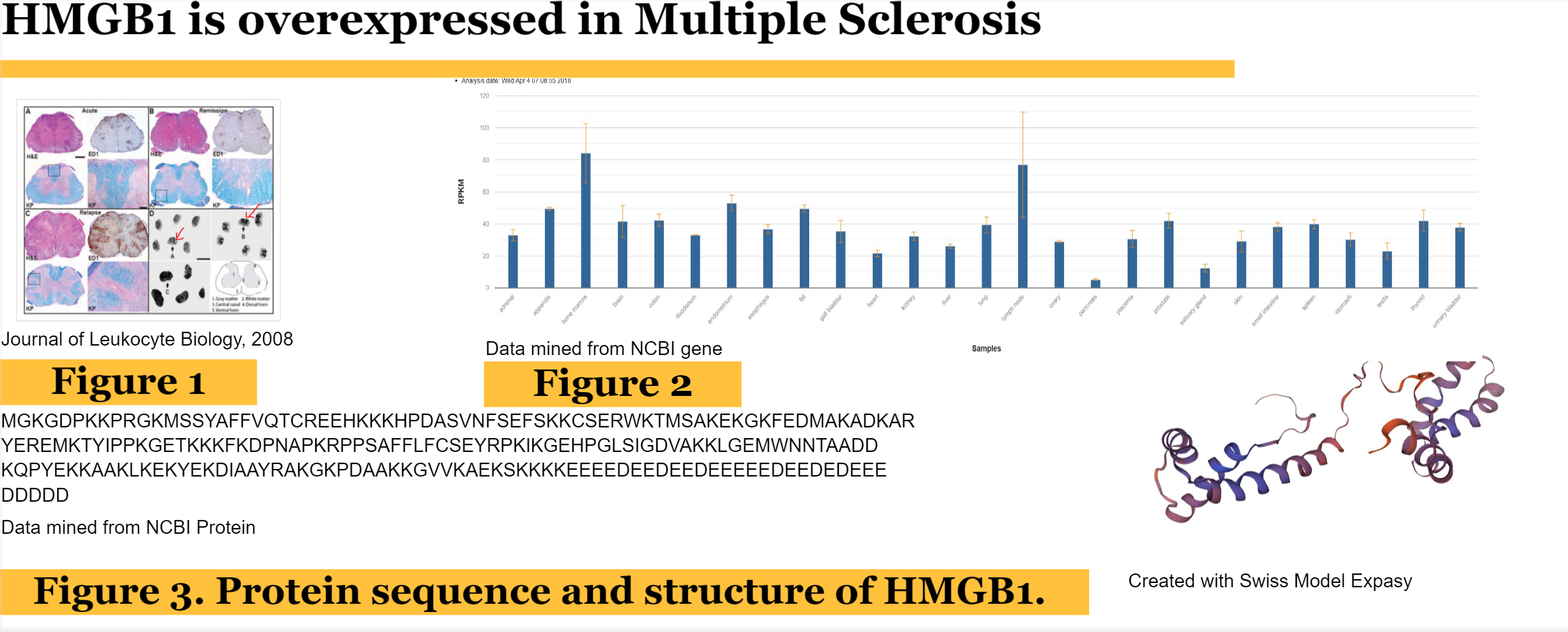
Click Start Modeling on the front page, add the FASTA sequence, click build model. Figure 3b.



Instructors may ask questions about the protein structure. A few examples are per course are listed:

General Biology  
Show the view of the secondary structures. How many secondary structures are there?  
Show the space filling model, ball and stick model, surface model, hyperball model, or cartoon model. There are 10 to choose from. Instructors may be interested in 1 or all.   
Biochemistry  
What is the Ramachandron %?  
Show a view of the hydrophobic residues.  
Show a view of the polar residues.

Create a visualization- a graphical abstract of the genomic, transcriptomic, and proteomic findings using Mind the Graph. Take a screen shot or snip and add to your report. Label as Figure 4.



Instructors may ask students which journal or conferences require graphical abstracts.

Add content to your CV/Resume in the skills and research experiences sections:

**Skills**

Mind the Graph Graphical Abstracts

Protein Modeling

Extraction of RNAseq Expression

Literature Review for Genomic associations

**Research Experience**

Performed literature review to determine abnormally expressed gene in condition X. Identified X expression among tissues with data extracted from NCBI gene. Analyzed RNA expression in X tissue related to X (a protein). Determined protein model of protein X in Swiss Model Expasy Pro. Examined the resulting X (ball and stick, space filling, etc.) model. Created a graphic abstract to communicate results.

Find a REU and apply

Search [here](https://www.nsf.gov/crssprgm/reu/reu_search.jsp) for REUS to apply for. Use the keyword search bar at the end of the webpage. Use genomics, transcriptomics, proteomics as keyword to find a REU in a state you are interested in.