**These queries can be typed within the window of MySQL or on the terminal (once connected to MySQL).**

**The first option is easiest. However, if you want to get all your information through terminal, you can follow the following commands to get connected to MySQL on terminal.**

1. Type everything after the dollar sign into terminal: $ mysql -u root -p
2. Enter password: [ You will be prompted to enter your password ] **Type in the password for your computer.**
3. **You should see something that looks like the following:**

Welcome to the MySQL monitor. Commands end with ; or \g.

Your MySQL connection id is 32

Server version: 5.7.27-ndb-7.6.11-cluster-gpl MySQL Cluster Community Server (GPL)

Copyright (c) 2000, 2019, Oracle and/or its affiliates. All rights reserved.

Oracle is a registered trademark of Oracle Corporation and/or its

affiliates. Other names may be trademarks of their respective

owners.

**EPITOPE DATABASE**

**paper\_library table**

***# Select all columns from this library***

**SELECT \* FROM EpitopeDatabase.paper\_library;**

***# Select author column***

**SELECT author FROM EpitopeDatabase.paper\_library;**

***# Select all columns where the num\_pep column is >100***

**SELECT \* FROM EpitopeDatabase.paper\_library WHERE num\_pep > 100;**

**paper\_library table**

***# Select all columns from this library***

**SELECT \* FROM EpitopeDatabase.peptide\_library;**

***# Select access\_num column from this library***

**SELECT access\_num FROM EpitopeDatabase.peptide\_library;**

***# Select all from this column where length > 5 and HLA\_class = I***

**SELECT \* FROM EpitopeDatabase.peptide\_library**

**WHERE length > 5 AND HLA\_class = "I";**

**surfacepep\_papers table**

***# Select all columns from this library***

**SELECT \* FROM EpitopeDatabase.surfacepep\_papers;**

***# Select the first\_author, journal, and year columns where the assay = immunoaffinity and data = yes***

**SELECT first\_author, journal, AND year FROM EpitopeDatabase.surfacepep\_papers**

**WHERE assay = “immunoaffinity” and data = “yes”;**

**PEPTIDE DEGRADATION DATABASE**

**experiment\_data table**

***# Select all columns from this library***

SELECT \* FROM PeptideDegradationDatabase.experiment\_data;

*# Select all columns where intensity = 4000000*

SELECT \* FROM PeptideDegradationDatabase.experiment\_data

WERE intensity > 4000000;

**experiments table**

***# Select all columns from this library***

SELECT \* FROM PeptideDegradationDatabase.experiments;

*# Select all columns where cell\_type = mac*

SELECT \* FROM PeptideDegradationDatabase.experiments WHERE cell\_type = “mac”;

**original\_peptides table**

***# Select all columns from this library***

SELECT \* FROM PeptideDegradationDatabase.original\_peptides;

*# Select the oripep\_seq column where protein = Gag*

SELECT oripep\_seq FROM PeptideDegradationDatabase.original\_peptides

WHERE protein = “Gag”;