DIFFERENTIAL GENE EXPRESSION ANALYSIS

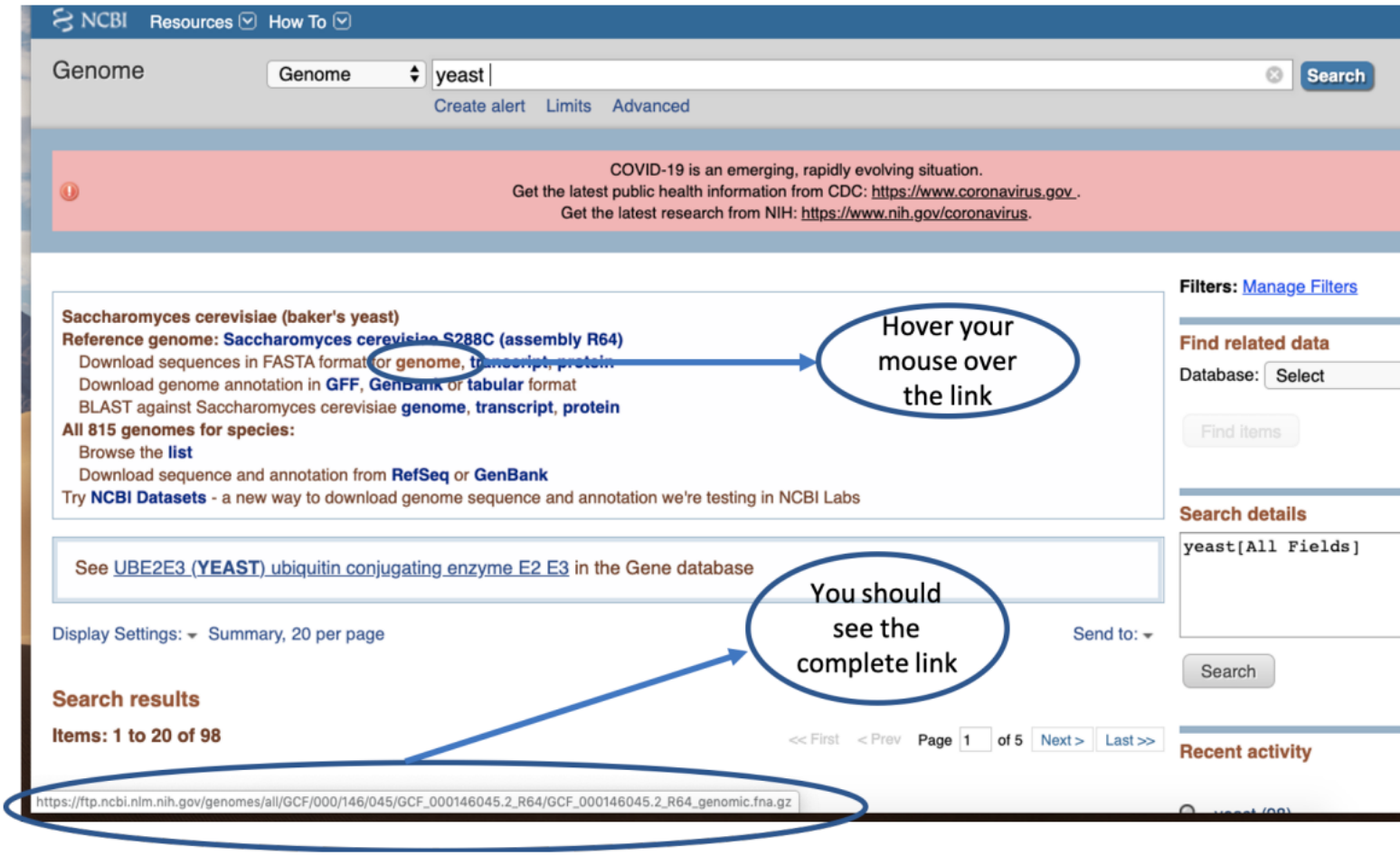
Module 2: Genome (.fasta) and annotation (.gff) file downloads

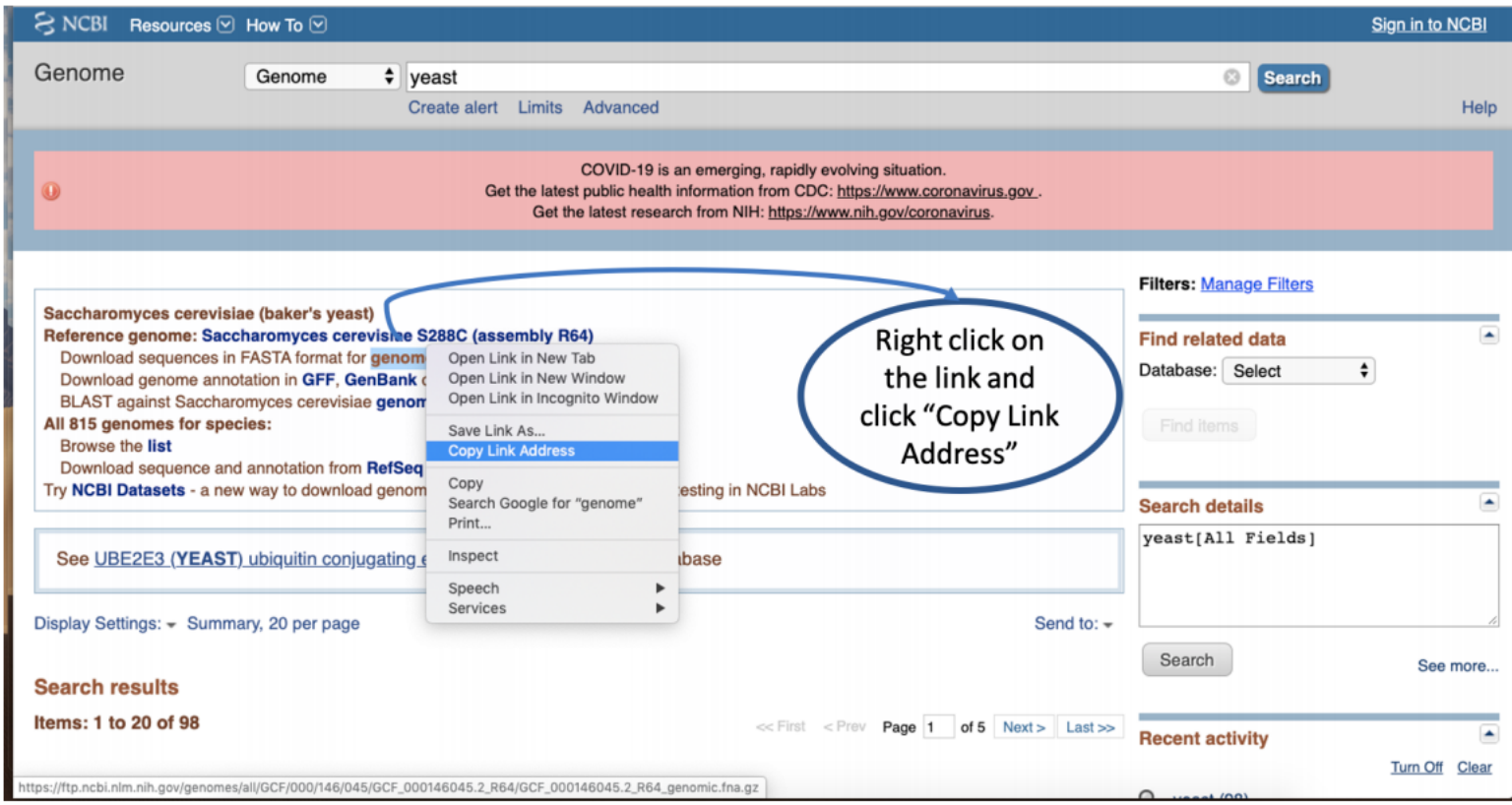
DOWNLOADING GENOME AND ANNOTATION FILES FROM PUBLIC DATABASES

```
# The human Genome can be downloaded from several public web portals.

# Gencode is a good option, with a clean and clear webpage:
# https://www.gencodegenes.org/human/
# Another is NCBI:
# https://www.ncbi.nlm.nih.gov/genome/?term=txid9606[orgn]
# To download the genome sequence in FASTA file format

cd /home/$USER/DGE_Virtual/

mkdir human_reference/

cd human_reference/
```

To get the download link to use in the "wget" command, do the following steps,

STEP 1: Go the relevant web page from where the genome fasta should be downloaded





STEP 2: Once the link has been copied, return to your Logrus session and execute the wget command

```
# wget command enables you to download files from the web directly to your server.
#A useful command to download genome fasta and annotation files from publicly available databases.

wget ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_human/release_29/GRCh38.p12.genome.fa.gz

# gunzip is used to extract the contents within a zipped file (uncompress).

gunzip GRCh38.p12.genome.fa.gz

# The above file will contain the nucleotide sequence of all regions in the GRCh38.p12 assembly.

# To download the genome annotation in a GFF3 file format

wget ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_human/release_29/\
gencode.v29.chr_patch_hapl_scaff.annotation.gff3.gz

gunzip gencode.v29.chr_patch_hapl_scaff.annotation.gff3.gz

# The above file will contain comprehensive gene annotation on the reference chromosomes,
# scaffolds, assembly patches and alternate loci (haplotypes) within the genome level assembly.
```

IN-CLASS EXERCISE TO NAVIGATE THROUGH SOME DATABASES TO DOWNLOAD GENOME AND ANNOTATION FILES

There are several publicly available databases that store genome and annotation files, including ENSEMBL, TAIR, Flybase, etc. While some genomes are resolved to the chromosome level, such as those of model organisms, many others have only a draft assembly available.

ACTIVITY 1 (download assigned genome and annotation files from NCBI)

In the following activity, you will download genomes and the associated annotation file for the assigned organism from NCBI using the command wget.

```
# Create a folder in your workspace called activity_1

cd /home/$USER/

mkdir activity_1

cd activity_1

# Make a directory called "reference" and download your genome into that folder

mkdir reference

cd reference

wget "paste the link here"
```