

Name: Ahmed Mahmoud Hussein
ID: 1180364

Task 2:

The file SGD_features.tab file contains the annotations for genomic features of the Yeast genome. The feature type is stored in the second column.

- Extract the feature types and pick a feature type that is unfamiliar to you. Look up its definition. Describe this feature and its relationships to other features.

Ans: ORF

long terminal repeat

ARS

tRNA gene

transposable element gene

snoRNA gene

LTR retrotransposon

telomere

rRNA gene

ncRNA gene

centromere

pseudogene

matrix attachment site

origin of replication

blocked reading frame

snRNA gene

non transcribed region

gene group

silent mating type cassette array

intein encoding region

telomerase RNA gene

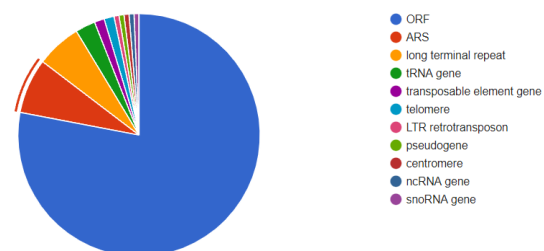
recombination enhancer

mating type region

ARS : In budding yeast, certain

autonomously replicating sequences

(ARSs) initiate the replication as ORIs, maintaining the stability of chromosomes and plasmids during genome replication.



Select a gene of interest. This may be a gene that you use in your research. Alternatively, you may select from the 4th column of the SGD_features.tab file (make sure you select a verified gene product). **Ans: Gene: YKR042W**

- Is the gene annotated in the GO? You might want to use the [Quick Go](#) interface to do this. Other alternatives also exist. If not, take a note of that then go back to the selection step. **Ans: Yes annotated in the GO**

- Look up the functions associated with the selected gene.

Ans: Involved in aging, oxidative stress response, and in the regulation of mitochondrial biogenesis. Inactivation of UTH1 increases life span, leads to higher resistance to heat stress and against hydrogen peroxide, and increases sensitivity to the superoxide radical-generating drug paraquat and to copper. Also required for the selective autophagic degradation of mitochondria (mitophagy) in response to nitrogen starvation. Involved in the remodeling of the cell wall during the various phases of yeast culture development and under various environmental conditions and plays a role in septation. Involved in cell sensitivity to boric acid.

- Can you tell whether a function you found is unique to your gene or not? Is it a rare or a common (often observed) function? **Ans: Not unique similar to YJL116C & common**