~~PROJECT NAME~~

~~Identify SNPs in a certain region~~

Frequencies of SNPs

Pairs of sgRNAs

File options (patient data and requirements)

Query options and validation

Visualization (SNPs, exons, and guide pairs [arcs])

Sorting, filtering, and set selection

Microservices for AlelleAnalyzer and other scripts

Logging and monitoring

Spark or MapReduce, Airflow, and Kubernetes

Can be run locally, on a network, or in the cloud

~~GitHub~~

~~Flask~~

~~React~~

Allele Analyzer

Finish Website

Microsoft Azure (terminated on and renewed after December 31st)

UCSF Wynton HPC

**MUST BE DONE**

1. **~~Reference’s genomic sequence given 17:45894554-46028334 (genomic coordinates)~~**
2. **MAPT to 17:45894554-46028334 (genomic coordinates given a gene symbol)**
3. **Exons given 17:45894554-46028334 (exons given genomic coordinates)**

<https://www.ncbi.nlm.nih.gov/projects/genome/guide/human/index.shtml>

Write a Python script using a library and (probably) this data (GRCh38).

<https://github.com/Honeycomb/sgrna_tool>

