

1 One account, multiple projects

To keep GenSAS free and available to all users, we do have some [user limits](#). Please abide by them. But feel free to have multiple projects but remember that only seven jobs can run at one time across all projects.

2 Start with a good genome assembly

GenSAS does have some [restrictions on genome size](#). Highly fragmented genomes do not annotate well, and the more pieces equals more time to run the tools.

3 Gather species-specific data

The provided protein and nucleotide databases are large and will take forever to run, especially at the 'Align' step. Take the time to download species-specific fasta files from GenBank and upload those under the ['Evidence' step](#).

4 Be patient

GenSAS only has access to a portion of our computational cluster and sometimes jobs need to wait before they can start running. And remember that more genome pieces equals longer run times.

5 Run jobs and look at the results

Not all tools or combinations of data will provide good results. And running all possible jobs will just slow down your project. Look at the results and make smart decisions. If you want some advice, please [contact the GenSAS team](#).

6 If a job fails, let us know

If a job fails or appears stuck, please [contact the GenSAS team](#). Remember to include your username, the project name, and the job name. DO NOT delete the job.

7 Use the videos and User's Guide

The GenSAS team has written an extensive [User's Guide](#) and is making [user videos](#). There is a wealth of information and tips in these resources.

8 If you get stuck, contact us!

We are more than willing to offer some pointers. Please [contact the GenSAS team](#) and include your username and the project name.