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# RUNNING SCARF TO GENERATE SCAR MARKERS

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This describes how to run the SCARF software to analyze two or more genome sequences and produce a file of candidate SCAR marker primer pairs for amplifying length-polymorphic regions of those genomes.

## **If not done already, download SCARF files:**

1. Browse to <https://github.com/BradyLab/SCARF>
2. In upper-left area of screen, find drop-down box Branch:master, click to open it, and choose the "release" branch.
3. At bottom of right column on screen, click "Download ZIP" and choose a place to put it on your computer.
4. Unzip the zip file on your computer.
5. Rename the unzipped folder from "SCARF-release" to just "SCARF".

## **If not done already, install SCARF:**

- Look inside the downloaded SCARF folder on your computer for file INSTALL.asciidoc and open it with a NotePad or TextEdit or other ASCII text editor and follow the installation instructions.

**To run SCARF and generate markers:** .