Scripps Research

Center for Computational Biology and Bioinformatics (CCBB)
2022

Have a sequencing project?
Follow the steps below for an effective and efficient outcome for your requests:

STEP1: Email Genomics Core Director, Steve Head, to discuss your proposed project and include CCBB if you are interested in Raw data / fastqs / data analyses. This step is critical to identify, allocate the right set of resources for good time/cost estimates.
      Tip: Share the biological context to your sequencing project (simple text or "Fig.1")

STEP2**: Submit request to Idea Elan database, Infinity, here for access to Genomics Core facility if this is your first sequencing project.

STEP3**: If you already have access to the Genomics Core facility, please login and submit SampleSubmissiom form available under the "Request Services" tab.
Need help? Email Sheila Roberts Weiland

STEP4: Samples can be submitted to the Genomics Core facility during the office hours on weekdays. Coordinate with John or Jessica or Nick to leave your samples in the freezer near the front door of the facility:
Building Name: Skaggs Institute For Chemical Biology, Campus map
MB-28, 10596 N. Torrey Pines Rd., La Jolla CA 92037

STEP5: If you plan on receiving raw data on a hard drive, deposit with Genomics Core facility an external hard drive with enough space on it at the time of sample submission.

STEP6: (Non-Scripps) External customers requesting fastqs and/or results of analysis (any processed data) must create an AWS S3 bucket with specifications provided here and share the requested details with CCBB at the time of sample submission.

STEP7: Consult our services page and click the relevant service type to get a quick glance at the timelines/costs involved (in terms of number of hours for CCBB effort) for completing your requests.

STEP8: Follow the "Recommended Guidelines for Authorship on Manuscripts"
STEP9: Please give us your feedback to better serve your sequencing needs!!

** STEPS 2 and 3 apply to internal (Scripps) customers only.