

# Successful Startup Request

---

**Title:** Impact of Helitron amplification on the genome architecture of *Myotis lucifugus*, the little brown bat

**Primary Field of Science:** Genetics and Nucleic Acids Science

**Resources Request Information:**

- What percentage of the work you expect to do in this allocation will be the following types:
  - Production (actually doing research): 100%
  - Exploration/porting (preparing to do research): 0%
  - Education (teaching others to do research): 0%
- What percentage of the jobs you expect to run in this allocation will be the following types:
  - Submitted through command line/script: 50%
  - Submitted using Grid tools (such as GRAM): 25%
  - Submitted through a meta-scheduler: 25%
- Please estimate what percentage of the science runs you expect to perform in this allocation will be the following types:
  - Independent (a job that is not immediately connected to any other job - a job that is artificially broken into chunks by queue limits should still be placed this category): 25%
  - Independent but related (such as jobs that make up an ensemble or parameter sweeps): 25%
  - Tightly-coupled (multiple jobs that will run simultaneously): 25%
  - Dependent (multiple jobs such as in a workflow): 25%

**Resource Requested:** PSC SGI Altix UV (Blacklight)

**Resource Requested Amount:** 30,000 SUs

**Resource Awarded Amount:** 30,000 SUs

**Abstract:** Transposable elements (TEs) are pieces of DNA that can move from one location to another within the genome. They constitute a significant portion of many eukaryotic genomes and play an important role in shaping genomic architecture. Helitrons are a group of TEs that are capable of capturing and amplifying host genome sequences. We have identified Helitrons in little brown bat, *Myotis lucifugus* and several cases of Helitron mediated gene capture events. The captured fragments were amplified up to 1000 copies in the genome. We are interested in understanding how these Helitron amplified gene fragments have altered the transcriptome and also in identifying the novel genetic units that might have been created due to the Helitron activity. To this end, would like to employ Trinity to assist in the assembling of RNA-Seq data generated through illumina sequencing as single reads (forward and reverse).