

## **Research Assistant (Bioinformatics)**

---

Example of duties

Research in genome and RNA sequence data of *Drosophila* species, especially focusing on transposable elements and repetitive elements.

Maintain and organize digital data files.

Analyze NGS data obtained in laboratory and/or publicly available and visualize for publication

Build up pipelines for analyzing specific type of data generated in the lab.

---

Minimum knowledge, skills and abilities

Knowledge of bioinformatics, genetics, molecular biology, and cell biology. Bachelor's degree in Biology, Bioinformatics, Computational Biology, Genetics, or a related field.

Familiarity with next-generation sequencing (NGS) data analysis, particularly RNA-seq.

Linux/Unix, bash/sbatch scripting in a High Performance Computing (HPC) environment, R or Python (preferably R or both), and familiarity with, or ability to learn a wide range of bioinformatics tools.

---

Experience and Training

- Experience with transposable element quantification and analysis using tools such as TETranscripts, Telescope, SQuIRE, or RepeatMasker-based workflows is preferred.
- Experience analyzing repetitive genomic regions and transposable elements is preferred.
- Experience analyzing next-generation sequencing (NGS) data, including RNA-seq datasets, is desirable.
- Experience with long-read sequencing data analysis (e.g., PacBio or Oxford Nanopore technologies) is preferred.

---

Schedule

Flexible work schedule; hours are negotiable and may vary based on project needs and candidate availability.

---

Salary

\$ 24 hourly