



THE UNIVERSITY OF
WESTERN AUSTRALIA



HARRY PERKINS INSTITUTE
OF MEDICAL RESEARCH

POST-DOCTORAL POSITION - EPIGENOME EDITING COMPUTATIONAL GENOMICS

Epigenetics and Genomics Laboratory (Lister Lab)

Harry Perkins Institute of Medical Research

The University of Western Australia

- 2 year appointment
- Salary: Level A (\$92,497 p.a.) or Level B (\$97,310 - \$115,350 p.a.)
- [Job Reference # 500899](#)

A post-doctoral position is available for a computational biologist to undertake research in the area of targeted epigenome editing. The successful applicant will have the opportunity to lead the computational components of research projects using sequencing-based high-throughput single cell profiling techniques to develop, optimize and apply new mammalian epigenome editing tools. The appointee will collaborate closely with experimental biologists in the group and will lead the computational analysis and interpretation of genomic datasets, in addition to contributing to experimental design and project direction.

The Epigenetics and Genomics Laboratory ([Lister Lab](#)), located at the Harry Perkins institute of Medical Research and the University of Western Australia, is comprised of molecular, cellular and computational biologists, forming a multi-disciplinary group undertaking a diverse range of (epi)genomics research. We utilize genomic, computational, cellular, and molecular approaches in multiple systems to investigate cellular mechanisms that control the usage of information encoded in the genome, and their roles in cell function and development. We have a particular interest in characterization and manipulation of the epigenome and cell identity using genomic and synthetic approaches.

Candidates with a background in computational biology and experience in single cell genomics are encouraged to apply. Candidates should have a PhD in a relevant discipline (Bioinformatics, Computer Science, Molecular Biology, etc). Demonstrated expertise in at least one common programming language (e.g. R, Python, Perl, C++, Java) and software version control (e.g. GitHub) is essential. Previous experience in the analysis of high-throughput sequencing data (e.g. RNA-seq, CHIP-seq, DNA methylation, chromatin accessibility) and statistical modeling of high-dimensional data is highly desirable. An understanding of the experimental techniques underlying such genomics experiments is advantageous. This is a full-time position, initially for a period of two years, with the possibility of further extension. Full details of the responsibilities and selection criteria are outlined in the [Position Description](#).

Application process: All applications should be submitted by email directly to recruitment-hr@uwa.edu.au (also cc ryan.lister@uwa.edu.au) with the job reference number included in the subject line. Applications should include a current CV, a separate statement addressing the key selection criteria outlined in the Position Description, and a cover letter that describes the applicant's research interests and career goals.

For further information contact Ryan Lister (ryan.lister@uwa.edu.au)

Closing date: July 8, 2018