Month XX, XXXX

Ms. Jane A. Doe

Organization

Street Address

City Name, State 00000-0000

Dear Jane A. Doe:

The Molecular and Genomics Informatics Core would like to express its wholehearted support for the {Proposal} entitled “{Project Title}” being submitted by {Dr. Name} in the Department of {Department}.

The Molecular and Genomics Informatics Core provides high-throughput computational services and resources to internal and external research laboratories. These services are provided through pre-project consultations, development and management of reproducible analysis pipelines, data management support, continued longitudinal analysis assistance beyond publication state, and continued education opportunities.

The Molecular and Genomics Informatics Core currently leverages redundant computational resources to ensure appropriate and scalable hardware requirements as well as timely project delivery. This includes a 64-bit Linux custom-built workstation with 16-core AMD Threadripper 3.5GHz processor, 128GB RAM and Radeon 8Gb RX 5700XT GPU with software installed for the myriad of bioinformatics applications, as well as a workflow manager (Nextflow) and container managers (Docker/Singularity) for scalable and reproducible bioinformatics analysis. Additionally, the Core has access to the computing resources within the Rutgers Amarel Cluster maintained by the Rutgers Office of Advanced Research Computing. This includes dedicated nodes totaling an additional 184 cores Intel Xeon 2.5Ghz processors with 832Gb RAM and 4x Nvidia A100 GPU accelerators, as well as on-demand access with the total system in excess of 250 nodes with more than 6000 Cores/CPUs, nearly 40TB RAM, and several iterations of GPU acceleration with expanding high-performance parallel storage. Lastly, the Core can offer cloud compute options to meet any computational needs not met by in-house capabilities.

The staff at the Molecular and Genomics Informatics Core can lend expertise in a variety of workflows including but not limited to: Transcriptomics (bulk, single cell or single cell multi-modal), Genomics (variant calling, annotation, de novo assembly), Epigenetics (ATAC, WGBS, ChIP), and Amplicons (metagenomics, deep PCR products). These services can be offered through standard pipelines maintained for reproducibility, rigor, and field-specific best practices, or through custom developed workflows to answer any biological question. End point data is delivered with the most effective visualizations, with continued modifications and support provided through publication and beyond for continued studies. Through the combination of various data-sets and collaboration with local core facility experts, the Molecular and Genomics Informatics Core is furthermore uniquely positioned for multi-omics integration as a current frontier of exploration.

As the Director of our Core, I am pleased to support {Dr Name} in pursuit of the research objectives outlined in the proposal. Please feel free to reach out to me with any questions regarding our capabilities or support for the project under consideration.

Sincerely,



Alexander Lemenze, PhD