

Name of the investigator

Official Address

Dear Dr. **Name of the Investigator**,

I am writing enthusiastically to support your proposal, "Project Title." We can provide sequencing support through the Yale Center for Genome Analysis. We have established protocols to facilitate high-throughput Sequencing and library preparation using multiple platforms. We will collaborate with Dr Knight in the Yale Center for Genome Analysis to provide sequence data for analysis.

As the Director of YCGA, I am pleased to collaborate on this proposal with you and your colleagues. I will provide your team with the full support possible through this Center. This is an important work for the University and this Center and will be well supported.

The Yale Center for Genome Analysis (YCGA) is a state-of-the-art DNA Sequencing Center. This full-service facility uses various technologies to provide microarray and next-generation DNA sequence (NGS) analysis services using state-of-the-art technologies. The Center occupies approximately 7000 sq. ft. of laboratory space and has two Illumina NovaSeqs, one each of PacBio Sequel II, Element AVITI, and Illumina MiSeq sequencing systems. YCGA has also used the Oxford Nanopore single-molecule technology for over four years. Using the NGS at YCGA resulted in more than 1000 publications, including more than 60 articles in high-impact journals such as Science, Nature, and Cell. YCGA has extensive experience with single-cell and spatial technologies. We offer regular services for 10X library preparation for gene expression, PIP-Seq, ScATAC-Seq, and Multi-omics. We also have extensive experience in spatial transcriptomics using VISIUM, Curio, 10X Xenium, Nanostring CosMx, Atlasxomics spatial ATAC-Seq, and MERFISH. YCGA offers many services to study epigenetic aspects of cells using CUT-& Tag, ATAC-Seq, and HiC. We provide technical consultation, library preparation, sequencing, and data analysis for these services.

The data generated at the Center is analyzed and stored using dedicated 400 nodes/4000 processor /16 GPU cluster and ~5 PB storage. The sequencing core staff has over eight years of experience and is very well-trained in sample processing as well as the operation of the equipment. Samples are tracked using the LIMS system. Bioinformatics support is provided by seven Ph.D.-level bioinformatics staff.

Based on my own experience as a molecular biologist in using the latest genomics technologies in mechanistic research and experienced technicians at YCGA, we are always open for you to talk and brainstorm ideas, especially when it comes to designing incisive experiments to rigorously test the findings made with next-generation sequencing approaches. My expertise in genomics and epigenetics, gained during doctoral and postdoctoral research, will allow me to be a valuable facilitator.

I find this proposal exciting and compelling, and I look forward to working with you and your team in the near future. I wish you the best of luck with your application. I look forward to our continued cooperation on this interesting project and wish you the best of luck with your grant proposal.

Sincerely,

Bony De Kumar, PhD