

Pradeep Bompada

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▣ PROFILE SYNOPSIS

Highly skilled molecular biologist and bioinformatician with extensive experience in next-generation sequencing (NGS), genome editing, and multi-omics data analysis. Adept at designing and executing wet-lab experiments, including ChIP-seq, RNA-seq, and DNA methylation studies, and proficient in advanced bioinformatics workflows for single-cell and bulk sequencing datasets. Strong programming skills in R, Python, and Linux, with a proven track record of integrating multi-layered genomic data to uncover regulatory mechanisms, disease biomarkers, and therapeutic targets.

- Demonstrated ability to manage multiple high-impact projects simultaneously, resulting in 12 peer-reviewed publications and several manuscripts in preparation.
- Experienced in CRISPR/Cas9 genome editing, including lentiviral delivery, knockouts, and SNP modifications, combined with downstream functional assays.
- Skilled in analyzing high-dimensional datasets (scRNA-seq, scATAC-seq, multiome, Hi-C) and visualizing results for publication-ready figures.
- Strong interpersonal and collaborative skills; effectively work with cross-functional teams, mentor colleagues, and communicate complex data to diverse audiences.
- Quick learner with a positive, goal-oriented mindset and strong organizational, problem-solving, and analytical skills.
- Passionate about leveraging cutting-edge molecular biology and bioinformatics to drive discoveries and improve patient outcomes.

▣ CORE COMPETENCIES

✱ NGS Library Preparation (ChIP-Seq, RNA-Seq) ✱ NGS quality control analysis using bioanalyzer (Agilent TapeStation) ✱ NGS wetlab workflow (ChIP-Seq, RNA-Seq) ✱ PCR / RT-PCR / QPCR ✱ Animal Models, Animal Handling (FELASAB) ✱ In-vivo Techniques (e.g. administration of glucose for IPGTT) ✱ Isolation of Blood Cells ✱ Statistical Analysis ✱ NGS Data Analysis (ChIP-Seq, RNA-Seq, Single-Cell RNA-Seq, DNA-Seq) ✱ Data Interpretation and Visualization using Linux, R and python.

▣ EDUCATION

Jun 2021 – Jun 2022 || Data Science online courses from Dalarna University, Sweden
2020 || PhD in Molecular Biology from Lund University, Sweden
2015 || master's in molecular biology from Lund University, Sweden
2013 || bachelor's in biotechnology from GITAM University, India

PROFESSIONAL SUMMARY

Post-doctoral Researcher
University of Colorado

November 2024-Present

Engagements

- Next generation sequencing data analysis including multiome single cell data, RNA-seq, HiC, ATAC-seq, ChIP-seq, etc.

Current projects

- ▲ Projects related to the identification of epigenetic regulation of chromatin and transcription in childhood brain tumors, particularly high-grade gliomas such as diffuse intrinsic pontine glioma (DIPG)
- ▲ Studying how CDK12 affects gene expression in glioma cells and exploring potential therapeutic strategies.

Post-doctoral Researcher
City of Hope

June 2023-October 2024

Engagements

- CRISPR lenti-virus production and virus titration.
- Cancer drugs titration.
- Analysis publicly available NGS data mining to identify new gene targets and its regulation.

Projects Undertaken

- ▲ Identification of novel genes and mechanisms involved in Ewing Sarcoma mediating the therapeutic efficacy inhibitors.
- ▲ Investigating role of newly identified clock gene in adipogenesis.

Post-doctoral Researcher

Lund University

Nov 2022 – May, 2023

Engagements

- Developing in vitro models to study the effects of ceramide accumulation in macrophages. ▪ Handling patient samples.
- Collaborating with medical doctors to discuss potential therapeutic targets for atherosclerosis.

Projects Undertaken

- ▲ Investigating causes and consequences of ceramide accumulation in T2D plaques.

PhD Researcher

Lund University

Jun 2016 – Dec 2020

Engagements

- Developed knowledge and skills in latest techniques and applications in Molecular Epigenetics and delivered training in research techniques and methods to colleagues and students.
- Engaged in cell culture, genome editing, ChIP and RNA sequencing techniques while efficiently handling 3 projects simultaneously.
- Maintained scientific data and conducted exhaustive data analysis to arrive at actionable conclusions.
- Prepared high-quality papers for submission to peer-reviewed journals and conference proceedings while carrying out original, high-level individual and collaborative research with other team members.

Projects Undertaken

- ▲ Histone acetylation of glucose-induced thioredoxin-interacting protein gene expression in pancreatic islets
- ▲ Epigenetic and Transcriptomic landscapes of glucose-induced histone acetylation in pancreatic islets ▲ Identification of blood based epigenetic biomarkers in type 2 diabetes

Stipendium Student and Project Assistant

Lund University

Feb 2015 – May 2016

Engagements

- Developed target specific CRISPR guide RNA based on cell line, used different CRISPR delivery methods such as lentiviral transduction and generated several gene knock out cell lines with least off target effects.
- Devised economical ChIP-qPCR and ChIP-sequencing protocols by understanding and analyzing various commercial protocols.
- Liaised with the Principal Investigators to organize workload and research activities, using appropriate materials, facilities, and equipment.
- Assisted in planning and carrying out original research encompassing investigations leading to the discovery of new biomarkers for type 2 diabetes.

Project Undertaken

- ▲ *Epigenetic regulation of glucose-stimulated osteopontin (OPN) expression in diabetic kidney.*
- ▲ *Role of osteopontin and its regulation in pancreatic islets.*
- ▲

❑ RESEARCH SUMMARY

NEXT GENERATION SEQUENCING DATA ANALYSIS

- Proficient in analyzing high-dimensional single-cell datasets, including scRNA-seq, scATAC-seq, and scMultiome (RNA+ATAC) using R, Python, ArchR, Seurat, and Scanpy.
- Skilled in multi-omics integration, including chromatin accessibility, gene expression, epigenomic marks, and 3D genome structure (Hi-C).
- Demonstrated expertise in ChIP-seq, ATAC-seq, RNA-seq, DNA methylation, and CUT&Tag/CUT&RUN data processing and downstream biological interpretation.
- Strong command of data visualization, generating high-quality plots (UMAPs, genome tracks, peak heatmaps, motif enrichment plots, pseudotime trajectories, volcano plots) for publication-ready figures.
- Experienced in building reproducible pipelines using Linux, R, Python, Snakemake, and cloud/HPC workflows.
- Adept at quality control, preprocessing, batch correction, normalization, clustering, differential expression/accessibility, peak calling, enhancer-gene linkage, and pathway enrichment analyses.
- Capable of integrating long-read sequencing and short-read NGS datasets for structural variant detection, isoform analysis, and regulatory landscape mapping.
- Demonstrated ability to interpret multi-layer NGS data to identify disease biomarkers, regulatory networks, and therapeutic targets.

GENOME EDITING BY CRISPR

- Gained practical experience to optimally utilize available online tools to design guide RNA.

- Gained extensive knowledge about various CRISPR-Cas9 delivery mechanisms including lentiviral methods which assisted in selecting the best method for different projects.
- Achieved 3 different knock-out cell lines and SNP edits.
- Demonstrated proficiency in using CRISPR technology to discover novel genes, molecular mechanisms, biomarkers, drug targets.

NEXT GENERATION SEQUENCING

- Proficiency in developing cost- efficient ChIP-sequencing protocol and establishing the method in various cell lines e.g., pancreatic cells, blood monocytes, podocytes, and kidney tissue.
- Showcased know how in NGS library preparation.
- Acquired expertise in diverse NGS methods such as ChIP-seq, RNA-seq and DNA methylation to recognize multiple biomarkers and drug targets for type 2 diabetes.
- Gained skills to evaluate NGS data by Linux, R and python programming.

IN-VIVO / IN-VITRO STUDIES

- Managed diverse mammalian cell types such as pancreatic beta cells, liver cells, kidney cells, and human primary cells such as pancreatic islets, kidney podocytes with precision.
- Efficaciously applied genome editing techniques and next generation sequencing methods in different cell lines. ▪ Meticulously handled mice and extracted primary cells such as pancreatic islets and performed IPGTT.

MOLECULAR BIOLOGY TECHNIQUES

- Gained expertise in RT-qPCR, PCR, SDS-PAGE, ELISA, RIA etc and performed cell based functional assays to investigate the effects of genome editing.

☐ **Publication link:** [Link to publications](#)
