

# Saurav Kumar Choudhary

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## EDUCATION

<b>Institute of Bioinformatics   University of Georgia   Athens, Georgia, USA</b>	<b>Aug 2022 – Present</b>
Doctor of Philosophy (Ph.D. in Bioinformatics)	GPA: 4.0/4.0
<b>Indraprastha Institute of Information Technology   Delhi, India</b>	<b>Jul 2020 – June 2022</b>
Master's in technology in Computational Biology	GPA: 8.25/10
<b>Amity Institute of Biotechnology   Noida, India</b>	<b>Jul 2015 – Jun 2019</b>
Bachelor of Technology in Biotechnology	GPA: 7.02/10

## RESEARCH EXPERIENCE

<b>Institute of Bioinformatics   University of Georgia   Athens, Georgia, USA</b>	<b>Aug 2022 – Present</b>
Graduate Student Researcher (Bioinformatics)	
Advisor – Dr. Kaixiong Ye	
<ul style="list-style-type: none"><li>Integrated human atlas-scale scRNA-seq and scATAC-seq datasets with GWAS summary statistics using scDRS and SCAVENGE to prioritize trait-relevant cell types for PUFA metabolism.</li><li>Analyzed large-scale single-cell RNA-seq datasets from collaborators, performing QC, alignment, quantification, normalization, clustering, and differential expression analysis.</li><li>Conducting de novo chromosome-scale genome assembly and annotation of <i>Hymenolepis diminuta</i> using PacBio HiFi reads, including repeat masking, gene prediction, synteny analysis and BUSCO-based quality assessment.</li><li>Developing a single-cell RNA-seq atlas of <i>Hymenolepis diminuta</i> by clustering, annotating, and integrating cell populations across samples using large-scale scRNA-seq data.</li><li>Applying Deep learning-based framework to infer gene regulatory networks from single-cell multiome (scRNA-seq and scATAC-seq) data using atlas-scale human datasets.</li></ul>	
<b>Indraprastha Institute of information Technology   Delhi, India</b>	<b>Jun 2021- June 2022</b>
Student Researcher	
Advisor – Dr. Vibhor Kumar	
<ul style="list-style-type: none"><li>Developed pathway-based feature representations from scRNA-seq data to improve interpretability and reduce feature dimensionality for machine-learning models.</li><li>Applied machine-learning models to pathway-level scRNA-seq features to identify conserved signatures across stem cell types and enable robust cell-state prediction under batch effects.</li></ul>	
<b>Eminent Biosciences   Indore, India</b>	<b>Feb 2020 – July 2020</b>
Bioinformatics Analyst	
Advisor - Dr. Anuraj Nayarisseri	
<ul style="list-style-type: none"><li>Performed bulk RNA-seq differential expression analysis of MCF-7 breast cancer and normal samples using R-based workflows.</li><li>Built and executed reproducible NGS analysis scripts in Python, R, and Bash on Linux systems.</li></ul>	
<b>Amity Institute of Biotechnology   Noida, India</b>	<b>Jan 2019 – Apr 2019</b>
Student Researcher (Structural Bioinformatics)	
Advisor – Dr. Archana Chaturvedi	
<ul style="list-style-type: none"><li>Performed protein modeling, active site prediction, molecular docking, model visualization and ADMET property analysis for GCC-ECD receptor</li></ul>	
<b>CSIR- Institute of Genomics and Integrative Biology   New Delhi, India</b>	<b>Jan 2019 – Apr 2019</b>
Research Intern	
Advisor – Dr. S Ramachandarn	
<ul style="list-style-type: none"><li>Conducted text-mining of biomedical literature using R (pubmed.mineR) to curate candidate genes associated with Type 2 Diabetes.</li><li>Identified and reported 30 disease-associated genes with literature-based supporting evidence.</li></ul>	

## PUBLICATIONS

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- Fu Z, Huang Z, Xu H, Liu Q, Li J, Song K, Deng Y, Tao Y, Zhang H, Wang P, Li H, Sheng Y, Zhou A, Han L, Fu Y, Wang C, **Choudhary SK**, Ye K, Veggiani G, Li Z, August A, Huang W, Shan Q, Peng H. IL-2-inducible T cell kinase deficiency sustains chimeric antigen receptor T cell therapy against tumor cells. *J Clin Invest.* 2024 Nov 26;135(4):e178558. doi: 10.1172/JCI178558. PMID: 39589809; PMCID: PMC11827851.
- Yu W, Kastriti ME, Ishan M, **Choudhary SK**, Rashid MM, Kramer N, Do HGT, Wang Z, Xu T, Schwabe RF, Ye K, Adameyko I, Liu HX. The duct of von Ebner's glands is a source of *Sox10*<sup>+</sup> taste bud progenitors and susceptible to pathogen infections. *Front Cell Dev Biol.* 2024 Aug 23;12:1460669. doi: 10.3389/fcell.2024.1460669. PMID: 39247625; PMCID: PMC11377339.
- Gupta N †, **Choudhary SK** †, Bhagat N, Karthikeyan M, Chaturvedi A. In Silico Prediction, Molecular Docking and Dynamics Studies of Steroidal Alkaloids of *Holarrhena pubescens* Wall. ex G. Don to Guanylyl Cyclase C: Implications in Designing of Novel Antidiarrheal Therapeutic Strategies. *Molecules.* 2021 Jul 8;26(14):4147. doi: 10.3390/molecules26144147. PMID: 34299422; PMCID: PMC8305770.
- Qureshi S, Khandelwal R, Madhavi M, Khurana N, Gupta N, **Choudhary SK**, Suresh RA, Hazarika L, Srija CD, Sharma K, Hindala MR, Hussain T, Nayarisseri A, Singh SK. A Multi-target Drug Designing for BTK, MMP9, Proteasome and TAK1 for the Clinical Treatment of Mantle Cell Lymphoma. *Curr Top Med Chem.* 2021;21(9):790-818. doi: 10.2174/1568026621666210119112336. PMID: 33463471.

## SKILLS

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**Genomics & Transcriptomics:** Single-cell RNA-seq, Single-cell ATAC-seq, Spatial transcriptomics, bulk RNA-seq, Genome Analysis: Genome assembly and annotation, GWAS integration.

**Programming Languages:** R, Python

**Scripting:** Bash (UNIX shell)

**R & Bioconductor:** Seurat, DESeq2, ArchR, Tidyverse, dplyr, ggplot2, stringr

**Python Libraries:** Scanpy, NumPy, Pandas, Matplotlib, PyTorch, scikit-learn

**Workflow & Reproducibility:** Git version control, documented and reproducible analysis pipelines

**High-Performance Computing:** Linux-based HPC environments, SLURM workload manager, job scheduling and resource management

**Bioinformatics Tools:** Cell Ranger, STAR, HISAT2 (scRNA/RNA-seq); minimap2, Hifiasm, BRAKER3 (long-read assembly and annotation); GENESPACE (comparative genomics)

## HONORS & PROFESSIONAL DEVELOPMENT

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- Peer Reviewer, PLOS Pathogens
- Secretary, Indian Student Association, University of Georgia (2023–2024); secured funding and coordinated community events for the UGA campus.
- Selected Participant, Duke–Chen Institute Joint Boot Camp on AI & AI-Accelerated Medical Research, Duke University (May 2025)
- Selected Participant, UCLA Computational Genomics Summer Institute (CGSI), 2024
- Selected Participant (Top 25 nationally), B4: Young Scientist Development Course – Big Data in Life Sciences and Healthcare (Harvard University & IBAB, India)
- Recipient, GATE Fellowship (All India Rank 1117) – awarded for entire M.Tech program
- Awarded “Best Minimalistic Poster Design,” Institute of Bioinformatics (IOB) Spring Retreat, April 2025
- Genetics Retreat Poster Award – 4th Place, September 2025
- Poster presentations at the American Society of Human Genetics (ASHG), 2023–2025
- Completed, R Programming (Coursera – Johns Hopkins University)