

DEVISHI KESAR

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EDUCATION

German Cancer Research Center(DKFZ)

Doctor of Natural Science

October 2026

- **Relevant Skills:** Multi-modal data integration, analysis of ChIP-seq, DNA methylation, copy number variation (CNV)

Georgia Institute of Technology

Master's in Bioinformatics

December 2020

- **Relevant Skills:** Variant calling analysis, differential expression analysis, database systems management

Indraprastha Institute of Technology Delhi

Bachelor of Technology (Honors) in Computer Science and Engineering

Minor in Computational Biology

August 2019

- **Relevant Skills:** Machine Learning, statistical analysis, graph modeling, big data analysis

Heidelberg, Germany

University of Heidelberg

Atlanta, GA, USA

Delhi, India

SKILLS

Programming and Computational Skills: Python, Bash, R, Java, Scala, Regex, SQL, MATLAB

Tools and Platforms: Git, Hive, Cytoscape, RStudio, PyMol, Databricks, AWS, Spark, Docker, Google Cloud Services

PUBLICATIONS

- Chaturantabut, S., Oliver, S., Frederick, D.T., Kim, J., Robinson, F.P., Sinopoli, A., Song, T.Y., He, Y., Chang, Y.C., Rodriguez, D.J., Chang, L., **Kesar, D.**, Ching, M., Dzvurumi, R., Atari, A., Tseng, Y.Y., Bardeesy, N., Sellers, W.R., Identification of potent biparatopic antibodies targeting FGFR2 fusion driven cholangiocarcinoma. (2025). *The Journal of Clinical Investigation*
- Chang, L., Jung, N.Y., Atari, A., Rodriguez, D.J., **Kesar, D.**, Song, T.Y., Rees, M.G., Ronan, M., Li, R., Ruiz, P., Chaturantabut, S., Ito, T., Tienen, L.M., Tseng, Y.Y., Roth, J., & Sellers, W.R. Systematic profiling of conditional pathway activation identifies context-dependent synthetic lethalties. (2023). *Nature Genetics*
- Li, R., Klingbeil, O., Monducci, D., Young, M. J., Rodriguez, D. J., Bayyat, Z., Dempster, J. M., **Kesar, D.**, Yang, X., Zamanighomi, M., Vakoc, C. R., Ito, T., & Sellers, W. R. Comparative optimization of combinatorial CRISPR screens. (2022). *Nature Communications*
- Mulvaney, K. M., Blomquist, C., Acharya, N., Li, R., Ranaghan, M. J., O'Keefe, M., Rodriguez, D. J., Young, M. J., **Kesar, D.**, Pal, D., Stokes, M., Nelson, A. J., Jain, S. S., Yang, A., Mullin-Bernstein, Z., Columbus, J., Bozal, F. K., Skepner, A., & Sellers, W. R. Molecular basis for substrate recruitment to the PRMT5 methylosome. (2021). *Molecular Cell*.
- Mason, M.J., Schinke, C., Eng, C.L.P. et al. Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. *Leukemia* (2020) - **member of DREAM consortium**
- Yang, et al. Assessment of the Limits of Predictability of Protein and Phosphorylation Levels in Cancer. (2020), *Cell Systems* - **member of NCI-CPTAC-DREAM consortium**

MANUSCRIPTS IN PREPARATION

- Knoll, N., Masser, S., **Kesar, D.**, Bordas, B., Kania, N., Zagar, S., Rodriguez, D.J., Jen, J., He, Y., Li, G., Mensah, C., Chen, Z., Feng, B., Chokshi, M., Raghavan, S., Sellers, W.R. and Mulvaney, K.M., CRISPR-Drug Combinatorial Screening Identifies Effective Combination Treatments for MTAP null cancer
- Shirole, N., **Kesar, D.**, Lee, Y., Goodale, A., Syamala, S., Kukreja, S., Li, R., Qiu, X., Yu, W., Goldman, S., Cejas, P., Long, H., Adelman, K., Doench, J., Sellers, W.R. and Kaelin, W., Sustaining Cyclin D1 Expression Renders Kidney Cancer Cells HIF2-Independent
- Pal, D., Rodriguez, D.J., Robinson, F.P., Chang, L., Potter, D.S., **Kesar, D.**, Li, R., Tienen, L.M., Mulvaney, K.M., Jung, N.Y., Jain, S., Park, J., Letai, A. & Sellers, W.R., WSB2, a novel propeller domain containing E3 ubiquitin ligase for BIM regulates cellular apoptotic thresholds

RESEARCH EXPERIENCE

Pediatric glioma research lab, DKFZ

Heidelberg, Germany

Graduate student

October 2023 – Present

- Processed ChIP-seq data to identify transcription factor binding patterns and histone modifications in pediatric gliomas
- Integrated RNA-seq and ChIP-seq data to link super-enhancer regions with gene expression
- Conducted transcription factor motif analysis to explore regulatory elements driving tumor-specific pathways
- Performed methylation and copy number variation analyses to uncover genetic and epigenetic changes in tumor subtypes
- Leveraged deep variational autoencoders and MOFA analysis to integrate multi-modal data, uncovering new relationships
- Constructed a gene regulatory network, uncovering novel biomarkers associated with different glioma subtypes

Sellers Lab, Broad Institute of MIT and Harvard

Cambridge, MA, USA

Associate Computational Biologist

April 2021 – September 2023

- Processed and analyzed data for CRISPR paralog redundancy screens to find actionable biomarkers
- Executed antibody docking and structure prediction for antibodies using modeling softwares
- Performed ChIPseq data analysis to look at TF motif enrichment and single nucleotide resolution cut profile
- Detected alternate splicing events helping suggest PBM interaction requirement for PRMT5-dependent splicing events
- Analyzed data from mass spectrometry experiments conducted to identify novel E3 substrates

Georgia Institute of Technology

Atlanta, GA, USA

Graduate Research Assistant

August 2019- December 2020

- Benchmarked variant calling pipelines by comparison of performance of mappers and variant callers
- Cataloged genomic variants from Colombian populations and characterized their predicted functional impact
- Identified single variant disease associations using best practices from the American College of Medical Genetics
- Evaluated distribution of health-related genetic variants among populations from Colombia in light of their ancestry

EMD Sereno

Billerica, MA, USA

Bioinformatics Summer Intern

May 2020 – July 2020

- Developed Rshiny app to share isolated immune cell RNAseq from bulk breast cancer tumors with biological experts
- Discovered novel myeloid drug targets by leveraging differential expression and gene signature analysis
- Drove bioinformatics discovery by frequently presenting results to key stakeholders across multiple departments
- Identified actionable biomarkers supporting therapeutic remediation of immuno-oncology and autoimmune disease

POSTER PRESENTATIONS

- **Kesar, D.**, Keck, M.K., Joshi, P., Okonechnikov, K., Autry, R.J., T.W. Jones, D.T.W., Integrated (epi)genomic atlas for identification of biomarkers in pediatric gliomas, KiTZ retreat 2024
- **Kesar, D.** Colombian Genome Diversity Project, GT@SC20 HPC Poster Show Proceedings
- **Kesar, D.** The discovery of context-specific paralog dependencies in cancer, Broad Retreat 2022

AWARDS

- Computational Biology Research Award – Spring 2020 and Fall 2020 – Georgia Tech
- Dean Academic Excellence Award – IIIT Delhi 2018
- RECOMB/ISCB Conference Travel Grant 2017

TEACHING EXPERIENCE

- Bulk RNA-seq computational analysis
 - Introduction to quantitative biology
- Instructor: Dr. Subhadip Raychaudhuri

Nov 2024-Present

Jan 2018-Apr 2018

LEADERSHIP AND VOLUNTEER EXPERIENCE

- Member, Social events team, DKFZ, Germany 2023-25
- Organizing team, Broad Retreat 2022, Broad Institute, USA 2021-22
- Volunteer, Charles river cleanup, The Charles River Conservancy, MA, USA, 2021-22
- Volunteer, GP Covid testing lab, Broad Institute, MA, USA, 2022

CERTIFICATIONS

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|-----------------------------------------------------------------------------------|--------|
| ● CRUK Children's Brain Tumor Centre of Excellence Summer School | Jul'24 |
| ● Cancer Genomics and Precision Oncology, online course by Harvard Medical School | Mar'22 |
| ● Immuno-oncology, online course by Harvard Medical School | Mar'22 |
| ● Precision medicine, online course by University of Geneva | Feb'21 |
| ● Starting single cell analysis, online course by EMBL-EBI | Jun'20 |
| ● Introduction to breast cancer, online course by Yale University | Jun'19 |
| ● Computer science and automation, Summer School IISc Bangalore | Jul'18 |
| ● Summer school in Bioinformatics NCBS | Jun'17 |