**DEVISHI KESAR**

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**EDUCATION**

**German Cancer Research Center(DKFZ) *Heidelberg, Germany***

*Doctor of Natural Science University of Heidelberg*

*October 2026*

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

**Georgia Institute of Technology *Atlanta, GA, USA***

*Master’s in Bioinformatics*

*December 2020*

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

**Indraprastha Institute of Technology Delhi *Delhi, India*** *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

**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 lethalities. (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 *Nov 2024-Present*

● Introduction to quantitative biology *Jan 2018-Apr 2018* Instructor: Dr. Subhadip Raychaudhuri

**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**

● 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