

# DEVISHI KESAR

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## EDUCATION

### German Cancer Research Center(DKFZ)

Doctor of Natural Science  
October 2026

Heidelberg, Germany  
University of Heidelberg

### Georgia Institute of Technology

Master in Bioinformatics  
December 2020

Atlanta, GA, USA

### Indraprastha Institute of Technology Delhi

Bachelor of Technology (Honors) in Computer Science and Engineering  
Minor in Computational Biology  
August 2019

Delhi, India

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## 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

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## PUBLICATIONS

- 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. (2025). *Cancer Discovery*
- 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**

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## MANUSCRIPT 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

## RESEARCH EXPERIENCE

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### **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
- Conducted transcription factor motif analysis to explore regulatory elements driving tumor-specific pathways
- Constructed a gene regulatory network, uncovering novel biomarkers associated with different glioma subtypes
- Leveraged machine learning and MOFA analysis to integrate multi-modal data, uncovering new relationships
- Performed single-cell analysis to trace biomarker expression and identify developmental blocks tied to tumor origin

### **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 Serono**

*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

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- **Kesar, D.**, Keck, M.K., Joshi, P., Okonechnikov, K., Autry, R.J., T.W. Jones, D.T.W., Deciphering pediatric glioma subtypes—Super-enhancer dynamics and (epi)genomic insights into cell of origin, Biology of Genomes, CSHL 2025
- **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, AACR 2025
- **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

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- 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

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

*Nov 2024-Present*

*Jan 2018-Apr 2018*

## LEADERSHIP AND VOLUNTEER EXPERIENCE

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- 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

## COURSES AND CERTIFICATIONS

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|---|--------|
| • Research Management Training for Early-Stage-Researchers                        | Apr'25 |
| • 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 |