Ashwini Kumar **Sharma, PhD**

Senior Principal Scientist - Computational Biology

Human Genetics and Genomics, GSK

https://ashwini-kr-sharma.github.io

Work Experience

2025 - present
SENIOR PRINCIPAL SCIENTIST
Human Genetics and Genomics, GSK

2021 - 2025
SCIENTIFIC INVESTIGATOR
Human Genetics and Genomics, GSK

- **Cross-functional Team Leadership, Strategic Planning & Project Management:** Worked in Matrix teams across multiple projects as the Computational Biology lead. Provided leadership to interdisciplinary projects. Influenced wet-lab experimental design, Planned & executed data analyses & computational biology experiments. Managed talent resourcing & delivery timelines. Performed risk assessment. Communicated key insights to senior leadership to impact decision-making on early target portfolios
- **Impacting early target portfolio:** Performed genomic & epigenomic evaluation and review of portfolio targets going into validation that directly impacted go/no-go decisions
- **High-throughput perturbation screens for early target discovery:** Computational Biology lead for functional genomics and chemogenomics perturbation screens in autoimmune and respiratory diseases. Have expertise in computational & statistical tools for analyzing -omics data generated from genome-scale and arrayed gene perturbation technologies like PerturbSeq/CROPseq, DRUGseq, 10x, and PARSE. Contributed to experimental design, performed computational data analysis, hit identification, perturbation signature identification & target mechanism of action evaluation studies
- **Building computational infrastructure for gaining key disease mechanism insights:** Created a robust & scalable Nextflow pipeline on Google Cloud Platform to perform partitioned heritability analysis. Generated the largest collection of disease-cell type associations (>1 million data points) based on the enrichment of disease heritability of >2000 GWAS studies in >2500 cell type-specific epigenomic profiles
- **Data visualization & Scientific communication:** Created a dynamic dashboard (Posit Shiny) to host results from various disease-mechanism association analyses performed in-house

Sep, 2016 - April, 2021
COMPUTATIONAL BIOLOGY SCIENTIST
Health Data Science Unit, University Hospital Heidelberg, Germany

- Identification of enhancer driven subtypes in neuroblastoma through integrative (epi-)genomic analyses
- Elucidating the developmental origins of neuroblastomas through single-cell genomic analyses
- Single cell RNA sequencing analysis of intestinal organoids in context of infection and interferon signalling
- Modelling Bayesian networks of epigenetic regulation across human tissues
- Computational phenotyping of signaling, transcription factors, metabolic pathways *etc* across tumors
- Screening for genes involved in redox homeostasis using chemical probes in the yeast mutant collection

Education

2011 - 2016
DOCTORATE IN NATURAL SCIENCES
German Cancer Research Center (DKFZ), Heidelberg, Germany
Hans Knöll Institute (HKI), Jena, Germany

- **Doctoral thesis:** *Computational analysis of metabolic reprogramming in tumors.*
  Established a novel computational workflow to identify metabolic genes co-altered with cancer-causing genes leading to dysregulation of the cancer cell metabolism landscape.
- **Collaboration projects:** Involved in 5 different collaborations with experimental groups as lead computational biologist in topics related to non-coding RNA, immunotherapy, biomarker discovery and mechanism of action of a chemotherapeutic drug. (See publications)

2009 - 2011 **MASTERS IN GENOMICS**
Madurai Kamraj University, Madurai, India

- **Project:** Structure-based rational design of a peptide inhibitor against *HIF1-HRE* binding and its structural studies. *Performed computational protein structure modeling and molecular dynamics studies.*
- **Internship: Center for Cellular and Molecular Biology, Hyderabad, India**
  Expression, purification, crystallization and *in-silico* modeling of the *FadD9* protein from Mycobacterium tuberculosis. *Performed cloning & transformation assays, protein isolation, western blotting, protein purification using chromatography techniques, protein crystallization and computational protein structure modeling.*

2006 - 2009 **BACHELORS IN BIOTECHNOLOGY**
Vellore Institute of Technology, Vellore, India

Technical Skills

https://github.com/ashwini-kr-sharma

- **Single cell analysis:** Expertise in single-cell data analysis - data QC, cell type annotation, cell marker identification, differential gene expression analysis, data integration, trajectory inference, transcriptional activity & gene regulation analysis *etc*
- **Genome scale pooled & Arrayed Perturbation screening data analysis:** Expertise in high-throughput screening technologies like PERTURBseq/CROPseq, DRUGseq, PARSE, 10x & CRISPR-FACS-based functional genomics screens. Have performed data analyses for Hit identification, Target mechanism of action evaluation, Perturbation signature scoring *etc*
- **Analysis of data generated from large public genomic and epigenomic datasets:** Expertise in analyzing data from RNAseq, CHIPseq, ATACseq, HiC, Methylation array, Microarray *etc*. Have worked extensively with data generated by consortium like TCGA, GTeX, ENCODE, BLUEPRINT, DepMap *etc*
- **Multi -omic data interpretation & integration:** Expertise in analysing data generated from various NGS technologies - Data clustering, Pattern identification, Differential expression/activity/abundance analysis, Pathway analysis, Regulatory network inference, Multi-modal data integration, Biomarker discovery, Scoring molecular signatures, Patient stratification, Associating signatures to clinical outcomes, Data visualization *etc*
- **Disease Genotype-to-Phenotype association studies:** Have expertise in integrating genetics (GWAS) and (epi-)genomics data using tools like sLDSC, MAGMA & scLinker to infer disease associated mechanisms
- **Machine Learning:** Expertise in applying supervised and unsupervised machine learning to NGS datasets - Non-negative matrix factorizations, data classification & feature selection *etc*
- **Reproducible research:** Have experience in Git, Github, Quarto, Rmarkdown, Plotly, Shiny, Nextflow, Snakemake, Docker
- **Coding/Tools:** Have experience in R statistical programming, Bioconductor, Python, Bash, Conda

Publications

https://goo.gl/tvIoC2

MY TOP FIVE SELECTED KEY PUBLICATIONS

1. Jansky S, **Sharma AK** , Körber V, Toprak UH, Gartlgruber M, Greco A, Quintero A, Chomsky E, Henrich K, Tanay A, Herrmann C, Höfer T, Westermann F. *Developmental programs in childhood neuroblastoma.* **Nature Genetics** (2021)
2. Gartlgruber M, **Sharma AK** , Quintero A, Dreidax D, Jansky S, Park Y, Gogolin S, Meder J, Doncevic D, Saary P, Toprak UH, Ishaque N, Afanasyeva E, Koster J, Versteeg R, Grünewald TGP, Jones DTW, Pfister SM, Henrich K, Nes Jv, Herrmann C, Westermann F. *Super enhancers define regulatory subtypes and cell identity in neuroblastoma.* **Nature Cancer** (2021)
3. Shukla K, **Sharma AK**, Ward A, Will R, Hielscher T, Balwierz A, Breunig C, Münstermann E, König R, Keklikoglou I, Wiemann S. *MicroRNA-30c-2-3p negatively regulates NF-B signaling and cell cycle progression through downregulation of TRADD and CCNE1 in breast cancer.* **Molecular Oncology** (2015)
4. Ansari SS, **Sharma AK**, Ali D, Eibl H, Soni H, Tews B, König R, Berger MR. *Induction of ER and mitochondrial stress by the alkylphosphocholine erufosine in oral squamous cell carcinoma cells.* **Cell Death and Disease** (2018)
5. **Sharma AK**, Eils R, König R. *Copy number alterations in enzyme-coding and cancer-causing genes reprogram tumor metabolism.* **Cancer Research** (2016)

MY OTHER PAPERS IN ORDER OF PERSONAL CONTRIBUTION

6. **Sharma AK**, König,R. *Metabolic network modeling approaches for investigating the "hungry cancer".* **Seminars in Cancer Biology** (2013)

7. Ansari SS., **Sharma AK**, Zepp M, Ivanova E, Bergmann F, König R, Berger M.R. *Upregulation of cell cycle genes in head and neck cancer patients may be antagonized by erufosine's down regulation of cell cycle processes in OSCC cells.* **Oncotarget** (2017)
8. Guo C, **Sharma AK**, Guzmán J, Herrmann C, Boulant S, Stanifer ML. *Interleukin-22 Promotes Cell Proliferation to Combat Virus Infection in Human Intestinal Epithelial Cells.* **Journal of Interferon and Cytokine Research** (2024)
9. Karkar S, **Sharma AK**, Herrmann C, Blum Y, Richard M. *DECOMICS, a shiny application for unsupervised cell type deconvolution and biological interpretation of bulk omic data.* **Bioinformatics Advances** (2024)
10. Khandelwal N, Breinig M, Speck T, Michels T, Kreutzer C, Sorrentino A, **Sharma AK**, Umansky L, Conrad H, Poschke I, Offringa R, König R, Bernhard H, Machlenkin A, Boutros M, Beckhove P *A high-throughput RNAi screen for detection of immune-checkpoint molecules that mediate tumor resistance to cytotoxic T lymphocytes.* **EMBO Molecular Medicine** (2015)
11. Ummanni R, Mannsperger HA, Sonntag J, Oswald M, **Sharma AK**, König R, Korf U. *Evaluation of reverse phase protein array (RPPA) based pathway activation profiling in 84 non-small cell lung cancer (NSCLC) cell lines as platform for cancer proteomics and biomarker discovery.* **Biochimica et Biophysica Acta (BBA)-Proteins and Proteomics** (2014)
12. Alvarez CR, Kee C, **Sharma AK**, Thomas L, Schmidt F, Stanifer ML, Boulant S, Herrmann C. *The endogenous cellular protease inhibitor SPINT2 controls SARS-CoV-2 viral infection and is associated to disease severity* **PLOS Pathogens** (2021)
13. Afanasyeva EA, Gartlgruber M, Ryl T, Decaesteker B, Denecker G, Mönke G, Toprak UH, Florez A, Torkov A, Dreidax D, Herrmann C, Okonechnikov K, **Sharma, AK**, Sagulenko V, Speleman F, .Henrich KO, Westermann, F. *Kalirin-RAC controls nucleokinetic migration in ADRN-type neuroblastoma.* **Life science alliance** (2021)
14. Triana S, Metz Zumaran C, Ramirez C, Kee C, Doldan P, Shahraz M, Schraivogel D, Gschwind AR, **Sharma AK**, Steinmetz LM, Herrmann C. *Single cell analyses reveal SARS‐CoV‐2 interference with intrinsic immune response in the human gut.* **Molecular Systems Biology** (2021)
15. Schwarz E, Alnæs D, Andreassen OA, Cao H, Chen J, Degenhardt F, Dwyer D, Eils R, Erdmann J, Herrmann C, Hofmann-Apitius M, Kaufmann T, Koutsouleris N, Kodamullil AT, Khuntia A, Munoz-Venegas ML, Nöthen MM, Paul R, Quintero A, Schunkert H, **Sharma AK**, Tost H, Westlye LT, Zhang Y, Meyer-Lindenberg A *Identifying multimodal signatures underlying the somatic comorbidity of psychosis: the COMMITMENT roadmap.* **Molecular Psychiatry** (2020)

Awards & Recognition

- **GSK Ahead Together Award** (2022)
  Given annually for most impactful work to the top 10% performers in the business unit
- **Global Recognition Awards (5 Bronze and 2 Silver) in my 3 years in GSK** (2021-24)
  For excellent performance, significantly exceeding targets and achieving key goals for the business
- Travel fellowship grant (2018)
  Spetses Summer School on Chromatin and Metabolism, from the ChroMe Network
- Helmholtz International Graduate School for Cancer Research Fellowship (2011-14)
  For pursuing doctoral training at DKFZ, Heidelberg
- CSIR-UGC-NET Junior Research Fellowship (2011) (declined)
  For pursuing doctoral training in India, presented by the Government of India
- Maveeran Sundaralingam Endowment Scholarship (2009-10)
  For securing highest grades during my Master's program
- ABLE-BEST 2010 entrepreneurship competition winners - 2nd best team in India (2010)
  For the project proposal - Nano beads-based diagnostic device for the detection of Tetanus neurotoxin using FRET
- Merit Endowment Award - (2007-08) and (2008-09)
  For excellent academic performance during my Bachelor's program

External collaborations & memberships

I am the **GSK Scientific lead** for the - *Open Targets Perturbation Catalogue* & *GSK EMBL-EBI Fibrosis project* and a member of the *International Society for Computational Biology (ISCB)*

Scientific Reviewer

I have served as (co-)/reviewer for research articles submitted in scientific journals like - *PLOS Computational Biology, BMC Systems Biology, NAR: Genomics and Bioinformatics and Scientific Reports, Immunoinformatics, Nature Communications*