

# ARASHDEEP SINGH

Post-doctoral researcher

 Bethesda (MD)



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## SUMMARY

Currently, I'm a postdoctoral fellow at the NCI-NIH, studying how alternative splicing and the tumor microenvironment drive development, progression, and therapy resistance in tumors using computational and bioinformatics tools. Next, I look forward to leverage my dual expertise in experimental and computational biology to uncover key principles and discover experimentally testable mechanisms in health and diseases.

## KEY PROJECTS AT NCI-NIH (Visiting Fellow, 2020 – Present)

### ❑ Analysis of embryonic alternative splicing in cancer

- **Summary** – We showed that alternative splicing in cancers significantly resembles their embryonic counterparts.
- **Publication** <https://www.nature.com/articles/s41467-022-35322-1>
- **Contribution** First Author

### ❑ Role of alternative splicing in resistance to MAPKi in melanoma

- **Summary** – Co-led this project and identified the transient alternative splicing events that enable the development of acquired resistance to MAPKi therapy in melanomas. Some of the findings from this work are undergoing experimental validation.
- **Publication (Abstract)** - <https://doi.org/10.1158/1538-7445.AM2024-LB250>
- **Contribution** Co-First author

### ❑ Computational pipeline for inferring clinically relevant cell state interactions

- **Summary** – Seeking inspiration from the concept of synthetic lethality, we developed a computational pipeline to identify cell state interactions in the IDH-mut glioma directly from bulk transcriptomic data.
- **Pre-print** - <https://doi.org/10.1101/2024.10.29.620901> - *Revised for Molecular Systems Biology*
- **Contribution** First Author

## KEY PROJECTS AT IISER-MOHALI (PhD Fellow, 2014 - 2019)

### ❑ Functional and evolutionary constraints underlying the 3D organization of genome

- **Summary** – Through the multivariate analysis of Hi-C with various functional and epigenomic datasets, we showed that genome 3D organization is shaped primarily by replication coordination and minimization of expression noise.
- **Publication** <https://academic.oup.com/dnaresearch/article/23/2/155/1745431>
- **Contribution** First Author

### ❑ Genome-wide discrepancy between binding and effect of chromatin factors

- **Summary** – We showed that transcriptionally non-functional binding of chromatin factors primarily mitigates genetic and epigenetic errors at their target sites, and I validated this through gene knockout experiments in budding yeast.
- **Publication (Abstract)** - <https://febs.onlinelibrary.wiley.com/doi/10.1002/1873-3468.13729>
- **Contribution** First author

## WORK EXPERIENCE

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### ❑ Visiting Research Fellow

- NIH (2020–Present)

### ❑ Teaching Assistant

- (BIO411 Bioinformatics Lab) – IISER Mohali

## SKILLS

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### ❑ NGS Data analysis

- End-to-end workflows for bulk RNA-Seq, Long read RNA-seq, Chip-Seq, HiC, and Mutation analysis.

### ❑ Single Cell RNA-seq Analysis

- Proficient in 10x and Smart-seq2 RNA-seq Analysis

### ❑ Scripting and Coding

- Proficient in R, PERL, and familiarity with Python.
- Shell scripting for automating analysis pipelines and computing on HPC

### ❑ Statistics and Data Analysis

- Data wrangling and visualization, Exploratory data analysis, Dimensionality reduction.
- Multivariate analysis, PCA, NMF, ICA.
- Machine learning, Regression, Classification, Hypothesis testing.

### ❑ Experimental Skills

- Light Field and Confocal Microscopy.
- Drosophila Genetics, Yeast Genetics, Gene Cloning
- Cell Culture: Bacteria, Budding Yeast, and Mammalian cancer cell lines.
- Molecular biology techniques like PCR, Agarose Gel Electrophoresis, SDS-PAGE, Immunostaining, X-Gal Staining etc.

## EDUCATION

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### ❑ PHD (Life Sciences)

- IISER Mohali (2014–2019)
- Thesis – Principles underlying the organization and function of yeast genome

### ❑ Dual BS-MS (Life Science)

- IISER-Mohali (2008-2013)
- Two years of college level science and mathematics with a majors in life-sciences

## AWARDS AND FELLOWSHIPS

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- ❑ EMBL Corporate Partnership Programme Travel Grant (Nov 2018)
- ❑ PhD Fellowship based on JGEEBILS Exam (2014-2019)
- ❑ KVPY Fellowship (2008-2013)

## REFEREES

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### ❑ Dr. Sridhar Hannenhalli

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## BIBLIOGRAPHY

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**\*denotes equal contributions.**

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- ❑ Mukherjee S\*, **Singh A\***, Joo H, Patiyal S, Kim H, Ray PL, Wang K. 2024. "Abstract LB250: Dynamics of Transcript Alternations and Differential Splicing in the Evolution of Acquired MAPKi Resistance in Melanoma". Cancer Research. doi:10.1158/1538-7445.AM2024-LB250.
- ❑ **Singh A**, Rajeevan A, Gopalan V, Agrawal P, Day CP, Hannenhalli S. Broad misappropriation of developmental splicing profile by cancer in multiple organs. Nat Commun. 2022 Dec 12;13(1):7664. doi: 10.1038/s41467-022-35322-1.
- ❑ **Singh A**, Choudhuri P, Chandradoss KR, Lal M, Mishra SK, Sandhu KS. Does genome surveillance explain the global discrepancy between binding and effect of chromatin factors? FEBS letters. 2020; 594(8) : 1339– 1353.. doi.org/10.1002/1873-3468.13729.
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- ❑ Ghosh S, **Singh A**, Mandal S, Mandal L. Active Hematopoietic Hubs in Drosophila Adults Generate Hemocytes and Contribute to Immune Response. Developmental Cell. 2015; 33(4) : 478– 488. doi : 10.1016/j.devcel.2015.03.014.
- ❑ Ruoff C, Mitchell A, Mondal P, Gopalan V, **Singh A**, Gottesman M, Hannenhalli S. Resistance signatures manifested in early drug response across cancer types and species. Cancer Drug Resist. 2025;8:44. <https://dx.doi.org/10.20517/cdr.2025.112>
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- ❑ Parkhitko AA, **Singh A**, Hsieh S, Hu Y, Binari R, Lord CJ, Hannenhalli S, Ryan CJ, Perrimon N. Cross-species identification of PIP5K1-, splicing- and ubiquitin-related pathways as potential targets for RB1-deficient cells. PLoS Genet. 2021 Feb 16;17(2):e1009354. doi:10.1371/journal.pgen.1009354.