# DISHA SHARMA

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https://www.linkedin.com/in/disha-sharma-514a5431/
12 years' experience in Bioinformatic analysis using R, Python, Bash, Machine Learning, Deep Learning, Cloud Computing, Statistics, CSS, HTML, MySQL

**Single Cell (Perturb-seq, Multiome, RNA, ATAC) | Bulk (WES, WGS, RNA, ATAC, Metagenome) | Cardiovascular Disorder | Rare Disease | Population Genomics | Big Data | Statistics Genetics | Machine learning | Deep Learning | Generative AI**

- **Software Engineering:** Accelerated 48 hrs human genome analysis to 6 hrs.
- **Pipeline Development:** Developed single-cell and bulk multi-omics, genomics pipeline with architecture using Nextflow, Docker, Snakemake and git version control.
- **Single cell Non-Coding:** First annotation of Cardiovascular lncRNA atlas in single-cell RNA dataset
- **Model Building:** Single-cell annotation using supervised machine learning model, Association Studies for Cardiometabolic disorders using UKBiobank and AllofUS.
- **Kaggle Competition:** Develop machine learning and deep learning models.
- **Database Development:** Build single cell and bulk databases using R, MySQL, HTML, and CSS.
- **Received 2020 BIRD award** for Bioinformatics and Functional Genomics

## PROFESSIONAL EXPERIENCE

**Post-Doctoral Fellow, Stanford University** **Dec. 2023 – Present**
**(Dr. Themistocles Assimes and Dr. Shoa L. Clarke Lab)**

- Performing GWAS (genome-wide association studies), building machine-learning based models and integrating single-cell multiomics using publicly available biomedical database and research resource including Million Veterans Program (MVP), UKBioBank, AllofUS, TopMed and GREGoR Consortium
- Using genomic foundation models to identify disease associated variants for clinical settings.

**Stanford Coursework Projects** **Dec. 2023 - Present**

BIODS271: Foundation Models in Healthcare

- **Report Data Summarization to Improve Radiology Workflows**

BIOD295: Generative AI in Healthcare

- **Skin Sight : Dermatology Triaging Platform utilizing Multimodal AI models**

**Post-Doctoral Fellow, Stanford University** **Sept 2020 – Nov. 2023**
**(Dr. Thomas Quertermous Lab)**

**Single-Cell Cardiovascular CRISPR perturbation**

- Understanding the molecular mechanism of cardiovascular disease using single-cell multi-omics from CRISPR gene perturbations. **Key Features:** *Single cell pipeline development & automation, Machine Learning modeling, Cloud Computing, Tap-seq analysis*, *Topic Modelling, Gene Regulatory Network (GRN)*
- CRISPR gene-perturbation in adipocytes using single cell multiome to identify the causal genes. **Key Features:** *Guide RNA design, Perturb-seq analysis, Power Calculation*
- Human Arterial Cell Atlas: *CZI Cell Atlas Initiative*

**Impact of Genome variations on disease and function with genome-wide association studies (GWAS)**

- Human cohorts and large-scale genome wide studies to identify genes, variations, and non-coding RNAs associated with coronary artery diseases. **Key Features:** *Population Genetics, Statistical Analysis, QTLs*

- Impact of genomic variations on functions (IGVF) using multi-omics data and regulatory network modelling. **Key Features:** *Predictive Modelling, Topic-modelling, Enhancer-Gene Regulatory Network, Deep Learning, GRN, Graphical Processing Unit (GPU)*

**Intel-India Fellow, Intel, Bangalore, India** **Sept 2019 – Aug 2020**

- Accelerate Clinical Analysis and Interpretation of Genomics Data through advanced tools/libraries. **Key Features:** *Software Engineering*, Cromwell work management system, Workflow Description Language (WDL), Slurm, workload manager, *Pipeline Development & Automation*

**Project Fellow and Graduate Student, CSIR-IGIB**, New Delhi, India **Nov. 2012 - July 2014**
**(Dr. Vinod Scaria's Lab)** **July 2014 - July 2019**

**SARS-CoV-2**

- Analysis of COVID-19 Sequencing datasets from Illumina and Nanopore sequencing to perform viral assembly and variant calling. **Key Features**: *Viral Genome assembly, variant calling, Big Data*

**Population and Disease Genomics**

- Analyzed whole genome sequencing of first >1,000 Indian individuals and annotated repeat expansion, structural variants, single nucleotide variants and small indels. **Key Features:** *Big Data, Genome Analysis pipeline*
- Genetic epidemiology of limb-girdle muscular dystrophy in Indian population. **Key Features:** *Ancestry Haplotyping, Natural Selection, Variant Classification*
- Genomics for understanding rare-diseases patients: Identification of disease-causing variants, copy number variation and repeat expansion in exome and genome sequenced patients. **Key Features:** *Variant Prioritization, Exome Analysis*

**Non-Coding RNA**

- Understanding the biology of circular RNAs using Zebrafish as model organism and created largest resources for circular RNA community. **Key Features:** *Circular RNA Atlas, Database development*
- Understand the role of non-coding RNAs (miRNAs, lncRNAs and lincRNA) in diverse biological datasets. **Key Features:** *Non-coding RNA analysis, Pipeline development and automation*

**Metagenome**

- Study of salivary oral metagenome in Autoimmune disorders. **Key Features:** *Microorganism Enrichment*

## TECHNICAL SKILLS

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| **Analysis** | Single Cell (CRISPR-Perturb, multiome, RNA, ATAC), Bulk (Genome, Exome, RNA, ATAC), Metagenome, Non-coding RNA analysis, Predictive Modelling, Gene Regulatory Network, Viral Genome Assembly, Variant Interpretation and Classification, GWAS-PheWAS, Mendelian Randomization (MR), Polygenic Risk Score Analysis (PGS). |
| **Programming** | R, Python, Bash, HTML, CSS, MySQL |
| **Key Tools** | Topic Modelling (Cistopics, cNMF, FastTopics), Gene Regulatory Network (pySCENIC, SCENIC+, MAGIC, FigR, Pando), Seurat, Signac, ArchR, CellRanger, Mutect2, GATK, limma, Nextflow, Snakemake DESeq2, EdgeR, ChromVar, HOMER, Monocle, LUMPY, R Shiny |
| **High Performance Computing** | Slurm, Sun Grid Engine, IBM Spectrum LSF |
| **Cloud Computing** | Amazon Web Services (AWS), Google Cloud Platform (GCP) |
| **OS Platform** | Linux (Ubuntu, RHEL), MacOS, Windows |
| **IDE** | Rstudio, VS Code, Jupyter Notebook, Google Colab |

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| **Workflow Manager** | Nextflow, Cromwell, Snakemake, Docker, Git version control |
| **Machine & Deep Learning** | scikit-learn, PyTorch, TensorFlow, Keras |

## EDUCATION

- **Ph.D.** in **Bioinformatics and Genomics**, CSIR-IGIB, 2014-2020
- **M.Sc.** in **Biotechnology**, Indian Institute of Technology Roorkee (IIT R), 2010-2012
- **B.Sc. in Biotechnology,** Banasthali University, 2007-2010

## Professional Positions

- **Postdoctoral Fellow in Stanford University,** 2020- Current
- **Intel India Fellow**, Intel India Pvt. Ltd. 2019-2020
- **Project Fellow** CSIR-IGIB, 2012-2014

## PROFESSIONAL CERTIFICATES

- Advance Language course in English; 2008
- Certificate Course in German Language; 2007
- Certificate Course in Music instrument Sitar;2007

## AWARDS & SCHOLARSHIP

- **National level Biotechnology Talent Search Examination 2011- Rank 136th**
- **CSIR-UGC National Eligibility Test (NET) -** All India Rank 58
- **Graduate Aptitude Test in Engineering (GATE) 2012 -** All India Rank 170
- **Indian Institute of Technology Joint Admission Test (IIT-JAM) –** All India Rank 51
- **Bio-Clues Innovation, Research and Development (BIRD) Award 2020**

## CONFERENCES & MEETINGS

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| • **Impact of Genome Variation on Function Consortium** | 09-2022 |
| • **CZI Virtual Seed Networks 2020 Annual** | 11-2020 |
| • **One Day Workshop: Data Science using R** | 12-2018 |
| • **SYNCON 2017-18 Bridging the Gap: Basic and Clinical Research from Bench to Bedside** | 01-2018 |
| • **NextGen Genomics, Biology, Bioinformatics and Technologies (NGBT) Conference** | 10-2017 |
| • **Workshop on Fundamentals of Systems Biology** | 12-2014 |
| • **Genomeet 2013** | 05-2013 |

## RESEARCH PAPER: 36 Published

1: Quertermous T, Li DY, Weldy CS, Ramste M, **Sharma D**, Monteiro JP, Gu W, Worssam MD, Palmisano BT, Park CY, Cheng P. Genome-Wide Genetic Associations Prioritize Evaluation of Causal Mechanisms of Atherosclerotic Disease Risk. **Arterioscler Thromb Vasc Biol. 2024** Feb;44(2):323-327. doi: 10.1161/ATVBAHA.123.319480. Epub 2024 Jan 24. PMID: 38266112.

2: **Sharma D**, Worssam MD, Pedroza AJ, Dalal AR, Alemany H, Kim HJ, Kundu R, Fischbein MP, Cheng P, Wirka R, Quertermous T. Comprehensive Integration of Multiple Single-Cell Transcriptomic Data Sets Defines Distinct Cell Populations and Their Phenotypic Changes in Murine Atherosclerosis. **Arterioscler Thromb Vasc Biol. 2024** Feb;44(2):391-408. doi: 10.1161/ATVBAHA.123.320030. Epub 2023 Dec 28. PMID: 38152886.

3: Imran M, Bhoyar RC, Jain A, Sahana S, Rophina M, Arvinden VR, Senthivel V, Divakar MK, Mishra A, Jolly B, **Sharma D**, Scaria V, Sivasubbu S. Genetic epidemiology of monogenic dyslipidemia and statin-associated adverse drug phenotypes in Indian population from whole-genomes of 1029 self-declared healthy individuals. **Human Gene 2024** Feb; doi: 10.1016/j.humgen.2023.201252

4: Verma D, Kapoor S, Kumari S, **Sharma D**, Singh J, Benjamin M, Bakhshi S, Seth R, Nayak B, Sharma A, Pramanik R, Palanichamy J. K. Sivasubbu S, Scaria V., Arora, M., Kumar, R., & Chopra, A. (2024). Decoding the genetic symphony: Profiling protein-coding and long non-coding RNA expression in T-ALL for clinical insights. **PNAS Nexus 2024**, gae011, doi: 10.1093/pnasnexus/pgae011

5: IGVF Consortium. The Impact of Genomic Variation on Function (IGVF) Consortium. **arXiv. 2023** July. doi: 10.48550/arXiv.2307.13708

6: Bielczyk-Maczynska E, **Sharma D**, Blencowe M, Saliba Gustafsson P, Gloudemans MJ, Yang X, Carcamo-Orive I, Wabitsch M, Svensson KJ, Park CY, Quertermous T, Knowles JW, Li J. A single-cell CRISPRi platform for characterizing candidate genes relevant to metabolic disorders in human adipocytes. **Am J Physiol Cell Physiol. 2023** Sep 1;325(3):C648-C660. doi: 10.1152/ajpcell.00148.2023. Epub 2023 Jul 24. PMID: 37486064; PMCID: PMC10635647.

7: Shi H, Nguyen T, Zhao Q, Cheng P, **Sharma D**, Kim HJ, Brian Kim J, Wirka R, Weldy CS, Monteiro JP, Quertermous T. Discovery of Transacting Long Noncoding RNAs That Regulate Smooth Muscle Cell Phenotype. **Circ Res. 2023** Mar 31;132(7):795-811. doi: 10.1161/CIRCRESAHA.122.321960. Epub 2023 Feb 28. PMID: 36852690.

8: Divakar MK, Jain A, Bhoyar RC, Senthivel V, Jolly B, Imran M, **Sharma D**, Bajaj A, Gupta V, Scaria V, Sivasubbu S. Whole-genome sequencing of 1029 Indian individuals reveals unique and rare structural variants. **J Hum Genet. 2023** Jun;68(6):409-417. doi: 10.1038/s10038-023-01131-7. Epub 2023 Feb 22. PMID: 36813834.

9: Kim HJ, Cheng P, Travisano S, Weldy C, Monteiro JP, Kundu R, Nguyen T, **Sharma D**, Shi H, Lin Y, Liu B, Haldar S, Jackson S, Quertermous T. Molecular mechanisms of coronary artery disease risk at the PDGFD locus. **Nat Commun. 2023** Feb 15;14(1):847. doi: 10.1038/s41467-023-36518-9. PMID: 36792607; PMCID: PMC9932166.

10: Weldy CS, Cheng P, Guo W, Pedroza AJ, Dalal, AR, Worssam MD, **Sharma D**, Nguyen T, Kundu R, Fischbein MP, Quertermous T. The epigenomic landscape of single vascular cells reflects developmental origin and identifies disease risk loci. **bioRxiv 2023** May. doi: 10.1101/2022.05.18.492517

11: Cheng P, Wirka RC, Kim JB, Kim HJ, Nguyen T, Kundu R, Zhao Q, **Sharma D**, Pedroza A, Nagao M, Iyer D, Fischbein MP, Quertermous T. Smad3 regulates smooth muscle cell fate and mediates adverse remodeling and calcification of the atherosclerotic plaque. **Nat Cardiovasc Res. 2022** Apr;1(4):322-333. doi: 10.1038/s44161-022-00042-8. Epub 2022 Apr 13. PMID: 36246779; PMCID: PMC9560061.

12: Bajaj A, Senthivel V, Bhoyar R, Jain A, Imran M, Rophina M, Divakar MK, Jolly B, Verma A, Mishra A, **Sharma D**, Deepti S, Sharma G, Bansal R, Yadav R, Scaria V, Naik N, Sivasubbu S. 1029 genomes of self-declared healthy individuals from India reveal prevalent and clinically relevant cardiac ion channelopathy variants. **Hum Genomics. 2022** Aug 5;16(1):30. doi: 10.1186/s40246-022-00402-2. PMID: 35932045; PMCID: PMC9354277.

13: Prakrithi P, Jha P, Jaiswal J, **Sharma D**, Bhoyar RC, Jain A, Imran M, Senthilvel V, Divakar MK, Mishra A, Scaria V, Sivasubbu S, Mukerji M. Landscape of Variability in Chemosensory Genes Associated With Dietary Preferences in Indian Population: Analysis of 1029 Indian Genomes. **Front Genet. 2022** Jul 12;13:878134. doi: 10.3389/fgene.2022.878134. PMID: 35903357; PMCID: PMC9315315.

14: Panda G, Mishra N, **Sharma D**, Kutum R, Bhoyar RC, Jain A, Imran M, Senthilvel V, Divakar MK, Mishra A, Garg P, Banerjee P, Sivasubbu S, Scaria V, Ray A. Comprehensive Assessment of Indian Variations in the Druggable

Kinome Landscape Highlights Distinct Insights at the Sequence, Structure and Pharmacogenomic Stratum. **Front Pharmacol. 2022** Jul 5;13:858345. doi: 10.3389/fphar.2022.858345. PMID: 35865963; PMCID: PMC9294532.

15: Sahana S, Bhoyar RC, Sivadas A, Jain A, Imran M, Rophina M, Senthivel V, Kumar Diwakar M, **Sharma D**, Mishra A, Sivasubbu S, Scaria V. Pharmacogenomic landscape of Indian population using whole genomes. **Clin Transl Sci. 2022** Apr;15(4):866-877. doi: 10.1111/cts.13153. Epub 2022 Mar 26. PMID: 35338580; PMCID: PMC9010271.

16: Prakrithi P, Singhal K, **Sharma D**, Jain A, Bhoyar RC, Imran M, Senthilvel V, Divakar MK, Mishra A, Scaria V, Sivasubbu S, Mukerji M. An *Alu* insertion map of the Indian population: identification and analysis in 1021 genomes of the IndiGen project. **NAR Genom Bioinform. 2022** Feb 15;4(1):lqac009. doi:10.1093/nargab/lqac009. PMID: 35178516; PMCID: PMC8846365.

17: Cheng P, Wirka RC, Shoa Clarke L, Zhao Q, Kundu R, Nguyen T, Nair S, **Sharma D**, Kim HJ, Shi H, Assimes T, Brian Kim J, Kundaje A, Quertermous T. *ZEB2* Shapes the Epigenetic Landscape of Atherosclerosis. **Circulation. 2022** Feb 8;145(6):469-485. doi: 10.1161/CIRCULATIONAHA.121.057789. Epub 2022 Jan 6. PMID: 34990206; PMCID: PMC8896308.

18: Jain A, Bhoyar RC, Pandhare K, Mishra A, **Sharma D**, Imran M, Senthivel V, Divakar MK, Rophina M, Jolly B, Batra A, Sharma S, Siwach S, Jadhao AG, Palande NV, Jha GN, Ashrafi N, Mishra PK, A K V, Jain S, Dash D, Kumar NS, Vanlallawma A, Sarma RJ, Chhakchhuak L, Kalyanaraman S, Mahadevan R, Kandasamy S, B M P, Rajagopal RE, Ramya J E, Devi P N, Bajaj A, Gupta V, Mathew S, Goswami S, Mangla M, Prakash S, Joshi K, Meyakumla, S S, Gajjar D, Soraisham R, Yadav R, Devi YS, Gupta A, Mukerji M, Ramalingam S, B K B, Scaria V, Sivasubbu S. Genetic epidemiology of autoinflammatory disease variants in Indian population from 1029 whole genomes. **J Genet Eng Biotechnol. 2021** Dec 14;19(1):183. doi:10.1186/s43141-021-00268-2. PMID: 34905135; PMCID: PMC8671593.

19: Roja Rani P, Imran M, Lakshmi JV, Jolly B, Afsar S, Jain A, Divakar MK, Suresh P, **Sharma D**, Rajesh N, Bhoyar RC, Ankaiah D, Shanthi Kumari S, Ranjan G, Anitha Lavanya V, Rophina M, Umadevi S, Sehgal P, Renuka Devi A, Surekha A, Chandra Sekhar P, Hymavathy R, Vanaja PR, Scaria V, Sivasubbu S. Insights from genomes and genetic epidemiology of SARS-CoV-2 isolates from the state of Andhra Pradesh. **Epidemiol Infect. 2021** Aug 3;149:e181. doi: 10.1017/S0950268821001424. PMCID: PMC8367868.

20: **Sharma D**, Sehgal P, Sivasubbu S, Scaria V. A genome-wide circular RNA transcriptome in rat. **Biol Methods Protoc. 2021** Sep 7;6(1):bpab016. doi:10.1093/biomethods/bpab016. PMID: 34527809; PMCID: PMC8435660.

21: Sahana S, Sivadas A, Mangla M, Jain A, Bhoyar RC, Pandhare K, Mishra A, **Sharma D**, Imran M, Senthivel V, Divakar MK, Rophina M, Jolly B, Batra A, Sharma S, Siwach S, Jadhao AG, Palande NV, Jha GN, Ashrafi N, Mishra PK, Vidhya AK, Jain S, Dash D, Kumar NS, Vanlallawma A, Sarma RJ, Chhakchhuak L, Kalyanaraman S, Mahadevan R, Kandasamy S, Devi P, Rajagopal RE, Ramya JE, Devi PN, Bajaj A, Gupta V, Mathew S, Goswami S, Prakash S, Joshi K, Kumla M, Sreedevi S, Gajjar D, Soraisham R, Yadav R, Devi YS, Gupta A, Mukerji M, Ramalingam S, Binukumar BK, Sivasubbu S, Scaria V. Pharmacogenomic landscape of COVID-19 therapies from Indian population genomes. **Pharmacogenomics. 2021** Jul;22(10):603-618. doi: 10.2217/pgs-2021-0028. Epub 2021 Jun 18. PMID: 34142560; PMCID: PMC8216321.

22: Radhakrishnan C, Divakar MK, Jain A, Viswanathan P, Bhoyar RC, Jolly B, Imran M, **Sharma D**, Rophina M, Ranjan G, Sehgal P, Jose BP, Raman RV, Kesavan TN, George K, Mathew S, Poovullathil JK, Keeriyatt Govindan SK, Nair PR, Vadekkandiyil S, Gladson V, Mohan M, Parambath FC, Mangla M, Shamnath A; Indian CoV2 Genomics & Genetic Epidemiology (IndiCovGEN) Consortium; Sivasubbu S, Scaria V. Initial Insights Into the Genetic Epidemiology of SARS-CoV-2 Isolates From Kerala Suggest Local Spread From Limited Introductions. **Front Genet. 2021** Mar 17;12:630542. doi: 10.3389/fgene.2021.630542. PMID: 33815467; PMCID: PMC8010186.

23: Ranjan G, Sehgal P, **Sharma D**, Scaria V, Sivasubbu S. Functional long non-coding and circular RNAs in zebrafish. **Brief Funct Genomics. 2021** Mar 23:elab014. doi: 10.1093/bfgp/elab014. Epub ahead of print. PMID: 33755040.

24: Jain A*, **Sharma D***, Bajaj A, Gupta V, Scaria V. Founder variants and population genomes-Toward precision medicine. **Adv Genet. 2021**; 107:121-152. doi:10.1016/bs.adgen.2020.11.004. Epub 2021 Feb 18. PMID: 33641745. (* co-first author)

25: Bhoyar RC, Jain A, Sehgal P, Divakar MK, **Sharma D**, Imran M, Jolly B, Ranjan G, Rophina M, Sharma S, Siwach S, Pandhare K, Sahoo S, Sahoo M, Nayak A, Mohanty JN, Das J, Bhandari S, Mathur SK, Kumar A, Sahlot R, Rojarani P, Lakshmi JV, Surekha A, Sekhar PC, Mahajan S, Masih S, Singh P, Kumar V, Jose B, Mahajan V, Gupta V, Gupta R, Arumugam P, Singh A, Nandy A, P V R, Jha RM, Kumari A, Gandotra S, Rao V, Faruq M, Kumar S, Reshma G B, Varma G N, Roy SS, Sengupta A, Chattopadhyay S, Singhal K, Pradhan S, Jha D, Naushin S, Wadhwa S, Tyagi N, Poojary M, Scaria V, Sivasubbu S. High throughput detection and genetic epidemiology of SARS-CoV-2 using COVIDSeq next-generation sequencing. **PLoS One**. 2021 Feb 17;16(2):e0247115. doi: 10.1371/journal.pone.0247115. PMID: 33596239; PMCID: PMC7888613.

26: Yadav SP, Thakkar D, Bhoyar RC, Jain A, Wadhwa T, Imran M, Jolly B, Divakar MK, Kapoor R, Rastogi N, **Sharma D**, Sehgal P, Ranjan G, Sivasubbu S, Sarma S, Scaria V. Asymptomatic reactivation of SARS-CoV-2 in a child with neuroblastoma characterised by whole genome sequencing. **IDCases**. 2021;23:e01018. doi: 10.1016/j.idcr.2020.e01018. Epub 2020 Dec 3. PMID: 33288996; PMCID: PMC7711173.

27: Jain A, Bhoyar RC, Pandhare K, Mishra A, **Sharma D**, Imran M, Senthivel V, Divakar MK, Rophina M, Jolly B, Batra A, Sharma S, Siwach S, Jadhao AG, Palande NV, Jha GN, Ashrafi N, Mishra PK, A K V, Jain S, Dash D, Kumar NS, Vanlallawma A, Sarma RJ, Chhakchhuak L, Kalyanaraman S, Mahadevan R, Kandasamy S, B M P, Rajagopal RE, J ER, P ND, Bajaj A, Gupta V, Mathew S, Goswami S, Mangla M, Prakash S, Joshi K, S S, Gajjar D, Soraisham R, Yadav R, Devi YS, Gupta A, Mukerji M, Ramalingam S, B K B, Scaria V, Sivasubbu S. IndiGenomes: a comprehensive resource of genetic variants from over 1000 Indian genomes. **Nucleic Acids Res. 2021** Jan 8;49(D1):D1225-D1232. doi: 10.1093/nar/gkaa923. PMID: 33095885; PMCID: PMC7778947.

28: Gupta V, Bhoyar RC, Jain A, Srivastava S, Upadhayay R, Imran M, Jolly B, Divakar MK, **Sharma D**, Sehgal P, Ranjan G, Gupta R, Scaria V, Sivasubbu S. Asymptomatic Reinfection in 2 Healthcare Workers From India With Genetically Distinct Severe Acute Respiratory Syndrome Coronavirus 2. **Clin Infect Dis. 2021** Nov 2;73(9):e2823-e2825. doi: 10.1093/cid/ciaa1451. PMID: 32964927; PMCID: PMC7543380.

29: Rophina M*, **Sharma D***, Poojary M, Scaria V. Circad: a comprehensive manually curated resource of circular RNA associated with diseases. **Database (Oxford). 2020** Jan 1;2020:baaa019. doi: 10.1093/database/baaa019. PMID: 32219412; PMCID: PMC7100626 (* co-first author).

30: GUaRDIAN Consortium; Sivasubbu S, Scaria V. Genomics of rare genetic diseases-experiences from India. **Hum Genomics. 2019** Sep 25;14(1):52. doi: 10.1186/s40246-019-0215-5. PMID: 31554517; PMCID: PMC6760067.

31: **Sharma D**, Sandhya P, Vellarikkal SK, Surin AK, Jayarajan R, Verma A, Kumar A, Ravi R, Danda D, Sivasubbu S, Scaria V. Saliva microbiome in primary Sjögren's syndrome reveals distinct set of disease-associated microbes. **Oral Dis. 2020** Mar;26(2):295-301. doi: 10.1111/odi.13191. Epub 2020 Jan 10. PMID:31514257.

32: **Sharma D**, Sehgal P, Mathew S, Vellarikkal SK, Singh AR, Kapoor S, Jayarajan R, Scaria V, Sivasubbu S. A genome-wide map of circular RNAs in adult zebrafish. **Sci Rep. 2019** Mar 5;9(1):3432. doi: 10.1038/s41598-019-39977-7. PMID: 30837568; PMCID: PMC6401160.

33: **Sharma D**, Sehgal P, Hariprakash J, Sivasubbu S, Scaria V. Methods for Annotation and Validation of Circular RNAs from RNAseq Data. **Methods Mol Biol. 2019**; 1912:55-76. doi: 10.1007/978-1-4939-8982-9_3. PMID: 30635890.

34: Sabharwal A, **Sharma D**, Vellarikkal SK, Jayarajan R, Verma A, Senthivel V, Scaria V, Sivasubbu S. Organellar transcriptome sequencing reveals mitochondrial localization of nuclear encoded transcripts. **Mitochondrion. 2019** May;46:59-68. doi: 10.1016/j.mito.2018.02.007. Epub 2018 Feb 24. PMID: 29486245.

35: Bhattacharjee J, Das B, **Sharma D**, Sahay P, Jain K, Mishra A, Iyer S, Nagpal P, Scaria V, Nagarajan P, Khanduri P, Mukhopadhyay A, Upadhyay P. Autologous NeoHep Derived from Chronic Hepatitis B Virus Patients' Blood Monocytes by Upregulation of c-MET Signaling. **Stem Cells Transl Med. 2017** Jan;6(1):174-186. doi: 10.5966/sctm.2015-0308. Epub 2016 Jul 28. PMID: 28170202; PMCID: PMC5442753.

36: Sandhya P, Danda D, **Sharma D**, Scaria V. Does the buck stop with the bugs?: an overview of microbial dysbiosis in rheumatoid arthritis. **Int J Rheum Dis. 2016** Jan;19(1):8-20. doi: 10.1111/1756-185X.12728. Epub 2015 Sep 19. PMID: 26385261.