Contact Information

National Cancer Institute, NIH
41 Medlars Dr, NIH Building 41
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Education and Training

Broad Institute of MIT and Harvard, Cambridge, MA

Postdoctoral Associate, Epigenomics Program   Dec 2018 - April 2024

- Advisors: Martin Aryee, Ph.D. and Alexander Meissner, Ph.D.
- Research Summary: Understanding the dynamics of gene regulation using single-cell genomics and long read sequencing

Baylor College of Medicine, Houston, TX

Ph.D., Quantitative and Computational Biosciences   Sept 2013 - Sept 2018

- Dissertation: Decoding Big Genomic Datasets: Biases, hypotheses & regulation
- Advisors: Zhandong Liu, Ph.D. and Kunal Rai, Ph.D.
- Advisory Committee: Zhandong Liu, Ph.D. (Chair), Huda Y. Zoghbi, M.D., Aleksandar Milosavljevic, Ph.D., Olivier Lichtarge, M.D., Ph.D., Mirjana Maletić-Savatić, M.D., Ph.D., Kunal Rai, Ph.D.

Carnegie Mellon University, Pittsburgh, PA

M.S., Computational Biology   Aug 2007 - Dec 2008

- Academic Achievement Fellowship (2007 - 2009)

Vellore Institute of Technology, Vellore, India

B. Tech, Bioinformatics   Aug 2002 - May 2006

- Dissertation: Host protein mimicry of *M. tuberculosis* proteins in *H. sapiens*
- Distinction with highest honors (equivalent to *summa cum laude*)

SELECTED PUBLICATIONS (* CO-FIRST AUTHORS)

1. E Orouji*, **AT Raman***, AK Singh*, ..., S Kopetz, K Rai. Chromatin state dynamics confers specific therapeutic strategies in enhancer subtypes of colorectal cancer. ***Gut*** (2022) (PMID: 34059508; DOI)

2. H Gu*, **AT Raman***, X Wang, AW Mohammad, A Arczewska, ZD Smith, DA Landau, MJ Aryee, A Meissner, A Gnirke. Smart-RRBS for single-cell methylome and transcriptome analysis. ***Nature Protocols*** (2021) (PMID: 34244697; DOI)

3. V Kochat*, **AT Raman***, ..., K Rai, KE Torres. Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. ***Acta Neuropathologica*** (2021) (PMID: 34283254; DOI)

4. **AT Raman***, AE Pohodich*, YW Wan, HK Yalamanchili, HY Zoghbi, Z Liu. Apparent bias towards long gene misregulation in MeCP2 syndromes disappears after controlling for baseline variations. **_Nature Communications_** (2018) (PMID: 30104565; DOI)

5. H Yi*, **AT Raman***, H Zhang, G Allen and Z Liu. Detecting hidden batch factors through data-adaptive adjustment for biological effects. **_Bioinformatics_** (2018) (PMID: 29617963; DOI)

HONORS AND DISTINCTIONS	• Hechter Memorial Travel Award, Broad Institute (2020)
	• Junior Research Parasite Award for Rigorous Secondary Data Analysis (2020)
	• MCBIOS Young Scientist Excellence Postdoc Award (Third place; 2020)
	• Gigascience Travel Award for Pacific Symposium on Biocomputing (2020)
	• GSBS Scholarship, Baylor College of Medicine (2013-2014)
	• Academic Achievement Fellowship, Carnegie Mellon University (2007-2009)
	• Undergraduate thesis awarded highest grade, Vellore Institute of Technology (2006)
	• Distinction with highest honors, Vellore Institute of Technology (2002-2006)

Research Experience

Staff Scientist   Apr 2024 - Present
LRBGE   Bethesda, MD
Center for Cancer Research, National Cancer Institute, NIH
Advisor: Dan Larson, Ph.D.

Statistical Epigenomics Postdoc Associate   Dec 2018 - Apr 2024
Epigenomics Program   Cambridge, MA
Broad Institute of MIT and Harvard
Advisor: Martin Aryee, Ph.D., Alexander Meissner, Ph.D.

Research Fellow   Jan 2022 - Present
Dept of Data Science, Dana Farber Cancer Institute   Boston, MA
Harvard Medical School (HMS)
Advisor: Martin Aryee, Ph.D. Collaborator: Bradley Bernstein, M.D., Ph.D.

Postdoc Associate   Jun 2019 - Present
Department of Pathology, Massachusetts General Hospital   Charlestown, MA
Harvard Medical School (HMS)
Advisor: Martin Aryee, Ph.D.

Research Assistant   May 2014 - Sept 2018
Jan and Duncan Neurological Research Institute   Houston, TX
Baylor College of Medicine
Advisor: Zhandong Liu, Ph.D.

Research Assistant   July 2015 - Sept 2018
Genome Medicine Department   Houston, TX
MD Anderson Cancer Center
Advisor: Kunal Rai, Ph.D.

Research Assistant   Jan 2014 - June 2015
Genome Medicine Department   Houston, TX
MD Anderson Cancer Center
Advisor: Lynda Chin, M.D.

Bioinformatics Scientist   July 2010 - July 2013
Institute for Systems Biology   Seattle, WA
Supervisors: Ilya Shmulevich, Ph.D.

Programming Analyst/ Statistician   April 2009 - July 2010
University of Pittsburgh   Pittsburgh, PA

Research Assistant   Oct 2007 - August 2008
Carnegie Mellon University   Pittsburgh, PA

**ALL
PUBLICATIONS**
(* CO-FIRST
AUTHORS)

Google Scholar H-Index = 19; Google Scholar i-Index = 19; **Scholar Link**

1. Antibody-drug Conjugates in Solid and Hematologic Malignancies. K Saleh, **A Raman**, M Zanoni. *Front Immunol.* (2025) (PMID: 40895559; DOI)

2. F Grizzi, M Martin-Perez, G Rai, AFUH Saeed, **A Raman**, D Bordoloi. Innate immune pathways as targets for developing therapeutic intervention against human cancers. *Front Immunol.* (2025) (PMID: 40416962; DOI)

3. H Guo*, J Vuille,*, B Wittner, E Lachtara, Y Hou, M Lin, T Zhao, **AT Raman**, ..., DA Haber. DNA hypomethylation silences antitumor immune genes in early prostate cancer and CTCs. *Cell* (2023) (PMID: 37327786; DOI)

4. CB Nava Lauson, S Tiberti, PA Corsetto, F Conte, P Tyagi, M Machwirth, S Ebert, A Loffreda, L Scheller, D Sheta, Z Mokhtari, T Peters, **AT Raman**, ..., Luigi Nezi, Teresa Manzo. Linoleic acid potentiates CD8+ T cell metabolic fitness and antitumor immunity. *Cell Metabolism* (2023) (PMID: 36898381; DOI)

5. E Orouji, **AT Raman**. Computational methods to explore chromatin state dynamics. *Briefings in Bioinformatics* (2022) (PMID: 36208178; DOI)

6. SC Callahan, V Kochat, Z Liu, **AT Raman**, J Schulz, C Terranova, M Divenko, A Ghosh, M Tang, C Pickering, J Myers, K Rai. High enhancer activity is an epigenetic feature of HPV negative atypical head and neck squamous cell carcinoma. *Frontiers in Cell and Developmental Biology* (2022) (PMID: 35927986; DOI)

7. E Orouji*, **AT Raman**, AK Singh*, ..., S Kopetz, K Rai. Chromatin state dynamics confers specific therapeutic strategies in enhancer subtypes of colorectal cancer. *Gut* (2022) (PMID: 34059508; DOI)

   - New Epigenetic Target May Lead to Personalized Treatments

8. CJ Terranova*, KM Stemler*, P Barrodia, SL Jeter-Jones, Z Ge, M de la Cruz Bonilla, **A Raman**, KL Allton, E Arslan, OH Yilmaz, MC Barton, K Rai, H Piwnica-Worms. Reprogramming of H3K9bhb at regulatory elements is a key feature of fasting in the small intestine. *Cell Reports* (2021) (PMID: 34818540; DOI)

9. V Kochat*, **AT Raman***, ..., K Rai, KE Torres. Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. ***Acta Neuropathologica*** (2021) (PMID: 34283254; DOI)

10. S Shareef, S Bevill, **AT Raman**, M Aryee, P Galen, V Hovestadt, B Bernstein. Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. ***Nature Biotech*** (2021) (PMID: 33958785; DOI)

11. H Gu*, **AT Raman***, X Wang, AW Mohammad, A Arczewska, ZD Smith, DA Landau, MJ Aryee, A Meissner, A Gnirke. Smart-RRBS for single-cell methylome and transcriptome analysis. ***Nature Protocols*** (2021) (PMID: 34244697; DOI)

12. C Terranova*, M Tang*, M Maitituoheti*, **A Raman**, ..., K Rai. Reprogramming of bivalent chromatin states in NRAS mutant melanoma suggests PRC2 inhibition as a therapeutic strategy. ***Cell Reports*** (2021) (PMID: 34289358; DOI)

13. **AT Raman**. A research parasite's perspective on establishing a baseline to avoid errors in secondary analyses. ***GigaScience*** (2021) (PMID: 33710326; DOI)

14. M Maitituoheti, EZ Keung, M Tang, L Yan, H Alam, G Han, **AT Raman**, ..., K Rai. Enhancer reprogramming confers dependence on glycolysis and IGF signaling in KMT2D mutant melanoma. ***Cell Reports*** (2020) (PMID: 33086062; DOI)

15. T Manzo, B Prentice, K Anderson, **A Raman**, ..., Giulio Draetta, Luigi Nezi. Accumulation of long-chain fatty acids in the tumor microenvironment drives dysfunction in intrapancreatic CD8+ T cells. ***Journal of Exp. Medicine*** (2020) (PMID: 32491160; DOI)

16. CA Chen, W Wang, SE Pedersen, **A Raman**, ..., HY Zoghbi, CP Schaaf. Nr2f1 heterozygous knockout mice recapitulate neurological phenotypes of Bosch-Boonstra-Schaaf optic atrophy syndrome and show impaired hippocampal synaptic plasticity. ***Hum Mol Genet.*** (2019) (PMID: 31600777; DOI)

17. S Adhikary*, D Chakravarti*, C Terranova*, I Sengupta, M Maitituoheti, A Dasgupta, D Srivastava, J Ma, **A Raman**, ..., K Rai, C Das. Atypical plant homeodomain of UBR7 functions as an H2BK120Ub ligase and breast tumor suppressor. ***Nature Communications*** (2019) (PMID: 30923315; DOI)

18. **AT Raman***, AE Pohodich*, YW Wan, HK Yalamanchili, HY Zoghbi, Z Liu. Apparent bias towards long gene misregulation in MeCP2 syndromes disappears after controlling for baseline variations. ***Nature Communications*** (2018) (PMID: 30104565; DOI)

    - Recommended by the Faculty of 1000
    - Synopsis in Texas Children's Hospital website: Long genes are not preferentially altered in Rett and MeCP2 duplication syndromes

19. C Terranova, M Tang, E Orouji, M Maitituoheti, **A Raman**, S Amin, Z Liu, K Rai. An integrated platform for genome-wide mapping of chromatin states using high-throughput ChIP-sequencing in tumor tissues. ***J Vis Exp.*** (2018) (PMID: 29683440; DOI)

20. H Yi*, **AT Raman***, H Zhang, G Allen and Z Liu. Detecting hidden batch factors through data-adaptive adjustment for biological effects. ***Bioinformatics*** (2018) (PMID: 29617963; DOI)

21. A Pohodich, HK Yalamanchili, **AT Raman**, YW Wan, M Gundry, S Hao, H Jin, J Tang, Z Liu, H Zoghbi. Forniceal deep brain stimulation induces gene expression and splicing changes that promote neurogenesis and plasticity. ***elife*** (2018) (PMID: 29570050; DOI). *Computational and Integrative analysis lead (equal contributor)*

    - Featured in TheScientist. Press release - Deep Brain Stimulation Affects the Activity of Hundreds of Genes

22. **AT Raman**, K Rai. Loss of histone acetylation and H3K4 methylation promotes melanocytic malignant transformation. ***Molecular & Cellular Oncology*** (2018) (PMID: 30250885; DOI)

23. U Oleksiewicz*, M Gladych*, **AT Raman***, ..., Kunal Rai, Maciej Wiznerowicz. TRIM28 and interacting KRAB-ZNFs control self-renewal of human pluripotent stem cells through epigenetic repression of pro-differentiation genes. ***Stem Cell Reports*** (2017) (PMID: 29198826; DOI)

24. The Cancer Genome Atlas Network. Genomic classification of cutaneous melanoma. ***Cell*** (2015) (PMID: 26091043; DOI)

25. V Litvak, A Ratushny, A Lampano, F Schmitz, A Huang, **A Raman**, A. Rust, A. Bergthaler, J. Aitchison, A. Aderem. A FOXO3-IRF7 gene regulatory circuit limits inflammatory sequelae of antiviral responses. ***Nature*** (2012) (PMID: 22982991; DOI)

    - Recommended by the Faculty of 1000

26. S Ramachandran, A Katiyar, A Sinha, A Bharadwaj, A Dutta, **A Raman** *et al.* Mycobacterium tuberculosis systems biology data in R. ***Biobytes, Indian Journal*** (2009) (URL)

PEER-REVIEW & PREPRINTS (* CO-FIRST AUTHORS)

1. ET Triglia*, TE Miller*, NC Durand, KL Kim, S Casani-Galdon, J D'Antonio, N Javed, AP Hernandez, **A Raman**, ..., BE Bernstein†, E Gaskell†. Chromatin topology and distal elements underlie divergent cell type-specific regulation of 9p21 locus cell cycle genes. ***In review, Cell Genomics*** (2025)

2. S Schiffers*, B Nelson*, M Prigge, S Krishna, Y Zhu, **A Raman** , Jingyao Ma, Hai-Quan Mao, Bin Wu†, Shalini Oberdoerffer†. ac4C enhances mRNA translation rate, fidelity and yield compared to N1-Methylpseudouridine. ***In revision, Nature (2024-10-21821)*** (2025)

3. A Nooranikhojasteh, G Tavallaee, N Khuu, S Yi Shen, S Ouladan, **A Raman**, Elias Orouji. Chromatin accessibility landscapes define stromal cell identities across tissues. ***In review, Communications Biology (COMMSBIO-25-6463)*** (2025)

4. M Maitituoheti*, E Arslan*, **AT Raman***, ..., K Rai. Pan-cancer Chromatin Landscape Reveals Principles of Epigenetic Heterogeneity and Dependencies in Cancer Cells. ***In revision, Nature Cell Biology (NCB-R44336)*** (2025)

5. CJ Terranova, M Maitituoheti, **AT Raman**, M Tang, ..., K Rai. H3K4me1-marked Enhancer Activation in Resistant Prostate Cancers Implicates SOX4 and MENIN Inhibition as Therapeutic Strategies. ***bioRxiv*** (2021) (DOI)

TEACHING
EXPERIENCE

- Co-Instructor for Introduction to data science (GPM705), HBKU Qatar (Jan-March, 2025)
    - Lead Instructor: Jithesh Puthen Veettil, Ph.D.
- Teaching Assistant for Bioinformatics Workshop, MD Anderson Cancer Center (Dec. 2017)
    - Supervised by Kunal Rai, Ph.D.
- Teaching Assistant for Computational Math for Quantitative Biomedicine, BCM
    - Supervised by Zhandong Liu, Ph.D. and Aleksandar Milosavljevic, Ph.D.
    - Evaluation from the students: **6/7** (Fall 2017)
- Taught a course on ChIP-seq analysis at ISB Nucleic Acid Course (2013)

GRANTS,
AWARDS &
MENTORSHIP

- American Society for Clinical Oncology Award ($50,000; 04/25-04/26)
    - Title: Uncovering the Role of NAT10 and Acetylation of RNA in Pancreatic Cancer (Awarded to Maria Farooq, M.D. (Postdoc, NIH))
    - Role: Co-Mentor/Biostatistician; helped designing the computational aims and provided the support letter
- Hechter Memorial Travel Award ($500; Broad Institute; 06/2020)
- Gordon and Betty Moore Foundation and Gigascience Travel Award ($3,500; 01/2020)
- GSBS Scholarship ($35,000; Baylor College of Medicine; 09/2013-09/2014)
- Academic Fellowship ($30,000; Carnegie Mellon University; 08/2007-12/2008)

SKILL-SET
SUMMARY

- **Next Gen-Sequencing Data Analysis**:
    - Proficiency in RNA-seq, ChIP-seq, ATAC-seq, Microarray, Detection and correction of Batch Effects, multi-omic analysis and data integration
    - Intermediate in scRNA-seq & scATAC-seq, Long-read seq, NanoString, GWAS & Fine-mapping analysis (PLINK, SuSie), RIP/Ribo/GRO/PRO-seq analysis
- **Programming Languages**:
    - Proficiency in R, Python, Perl
    - Intermediate in MATLAB, Shell Scripting, WDL
    - Familiarity in Octave, C/C++, Java
- **High Performance Computing**: Load Sharing Facility (LSF), Condor
- **Cloud Computing**: Google Cloud Computing, Terra
- **Operating Systems**: Linux, Windows, Mac OS X, Unix
- **Machine Learning Algorithms**: Clustering (k-means, hierarchical clustering, NMF, semi-NMF), Dimensionality reduction methods (PCA, ICA, t-SNE, UMAP, MDS), Classification Algorithms (Naive Bayes, Linear Discriminant Analysis, Decision Trees, Random Forest, SVM, Logistic Regression), Regression (Linear, GLM), Regularization (LASSO, Ridge, Elastic-net)

RESEARCH EXPERIENCE IN DETAIL	**Staff Scientist** Larson Lab, National Cancer Institute, NIH	April 2024 - Present Bethesda, MD

Staff Scientist — April 2024 - Present
Larson Lab, National Cancer Institute, NIH — Bethesda, MD

- Elucidate mRNA splicing patterns and chemical modifications of nucleotides using high throughput datasets
- Studying the role of RNA modification in frame-shifting
- Studying the exonization of transposon elements as a source of neo-tumor antigens

Statistical Epigenomics Postdoctoral Associate — Dec 2018 - April 2024
Aryee and Meissner Labs, Broad Institute of MIT and Harvard — Cambridge, MA

- Understanding the dynamics of gene regulation using single-cell genomics (Published in *Nature Protocol* and *Nature Biotechnology*) and long read sequencing
- Understanding the role of DNA methylation and its writers in diseases, development and aging
- Elucidating regulatory mechanisms of tumor suppressor genes in senescence (Calico)

Graduate Student / Research Assistant — Sept 2013 - Sept 2018
Liu's Lab, NRI, Baylor College of Medicine — Houston, TX
Rai Lab, Genome Medicine, MD Anderson Cancer Center

- Amplification-based expression data show bias towards long gene misregulation in synaptic disorders (Published in *Nature Comm.*)
- Developed batch detection algorithm in gene expression datasets (Published in *Bioinformatics*)
- Mechanism behind the effects of deep brain stimulation in Rett syndrome, meta-analysis of activity dependent genes and intellectual disorders (Published in *elife* and *Hum Mol Genet.*)
- Epigenomic landscape in colorectal tumors (Published in *Gut*)
- Oncogenic Role of EZH2 in the pathogenesis of MPNST tumors (Published in *Acta Neuropathologica*)
- Role for the TRIM28/KRAB repressors during early development, with a particular emphasis in nuclear reprogramming (Published in *Stem Cell Reports*)
- Lymphocytic Infiltration as a basis of response in melanoma tumors (Published in *Cell*)
- Multi-omics integrative analysis of ChIP-seq and RNA-seq datasets
- Genome wide analysis of non-coding regulatory mutations in cancer

Bioinformatics Scientist — July 2010 - July 2013
Shmulevich Lab, Institute for Systems Biology — Seattle, WA

- Rhinovirus vs Influenza Virus Project: Analyzing the similarities and differences between the two viruses using microarray datasets (Proctor & Gamble Project)
- Tol-II Receptors Project: Analysis of Pol-II, Transcription Factor, HDAc ChIP-seq datasets, Integrative analysis with gene Expression data for the discovery of gene regulatory network that gets activated in the presence of Tol-II receptors (Published in *Nature*)
- Poised Genes Project: Predicting poised genes in the macrophages using machine learning algorithms
- In-House ChIP-seq Pipeline: Development and integration of various functionalities

within the pipeline

Statistician   Nov 2009 - July 2010
Computational Genetics Lab, WPIC-UPMC   Pittsburgh, PA

- Palau Project: Analyzed GWAS datasets for the detection of causal genes in psychotic disorders and schizophrenia and
- Implemented genomic distance based multivariate regression model for the estimation of Identity by Descent (IBD) in the haplotype datasets
- Worked on the detection of IBD for the use of the population based linkage analysis among the case and control pairs

Research Assistant Programmer   Apr 2009 - Oct 2009
Department of Biomedical Informatics, University of Pittsburgh   Pittsburgh, PA

- Feature/covariates selection from comparative and high-throughput data for the prediction of protein-protein interaction pairs
- Computational prediction and accuracy of different statistical based algorithms such as discriminative and generative algorithms, and clustering based algorithms

Research Assistant   Sept 2007 to Dec 2007
Murphy Lab, Carnegie Mellon University   Pittsburgh, PA

- Development of database using PostgreSQL and JSP as back-end and front-end respectively

Research Trainee   Dec 2005 to Nov 2006
Institute of Genomics and Integrative Biology   New Delhi, India
Advisers: Dr. S. Ramachandran and Dr. Vani Brahmachari

- B.Tech Thesis: Study of Host Protein Mimicry of M. tuberculosis proteins in *H. sapiens*
- Comparative genomic analysis of *M. tuberculosis* H37Rv with *H. sapiens* using sequence and structural based approaches

INVITED
PRESENTATIONS
& SEMINARS

1. Amplification-based expression data show bias towards long gene misregulation in synaptic disorders in MeCP2 syndrome. Virtual/oral presentation for the Young Scientist Award session, *Annual Conference Of The Midsouth Computational Biology & Bioinformatics Society (MCBIOS) and MAQC Annual Meeting* (2020)

2. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *IGIB, New Delhi*. Host: Debasis Dash, Ph.D. and Anurag Agrawal, M.D., Ph.D. (2019)

3. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *Harvard Medical School, Boston*. Host: Steven McCarroll, Ph.D. (2018)

4. Deciphering epigenomic landscape in colorectal cancer at *Genome Medicine Science Day, MD Anderson Cancer Center*, Houston, TX (2018)

5. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *Broad Institute of MIT and Harvard, Cambridge*. Host: Evan Macosko, M.D., Ph.D. and Aviv Regev, Ph.D. (2018)

6. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *Broad Institute of MIT and Harvard, Cambridge*. Host: Martin Aryee, Ph.D., Alexander Meissner, Ph.D. and Andreas Gnirke, Ph.D. (2018)

7. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *University of Toronto, Toronto*. Host: Mathieu Lupien, Ph.D. (2018)

8. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *University of California, San Diego*. Host: Bing Ren, Ph.D. (2018)

9. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *University of California, Los Angeles*. Host: Daniel Geschwind, M.D., Ph.D. (2018)

10. ChIP-seq Analysis: Pipelines and Data Interpretations at *ISB Nucleic Acid Course*, Seattle, WA (2013)

ACADEMIC SERVICES & MEMBERSHIPS
- **Peer Review (*ad hoc*)**: Nature Communications, PLOS Computational Biology, IUBMB Life, Stem Cell Research & Therapy, Frontiers in Genetics, Frontiers in Immunology, Frontiers in Molecular Biosciences
- **Guest Editor**: Frontiers in Pharmacology, Frontiers in Immunology

REFERENCES
Zhandong Liu, Ph.D.
Associate Professor, Department of Pediatrics
Chief of Computational Sciences, Texas Children's Hospital
Jan and Dan Duncan Neurological Research Institute
Baylor College of Medicine, Houston, TX 77030
✉ zhandonl@bcm.edu

Huda Zoghbi, M.D.
Professor, Depts of Neuroscience, Molecular and Human Genetics,
Depts of Pediatrics and Neurology
Investigator, Howard Hughes Medical Institute
Jan and Dan Duncan Neurological Research Institute
Baylor College of Medicine, Houston, TX 77030
✉ hzoghbi@bcm.edu

Kunal Rai, Ph.D.
Professor, Dept. of Genome Medicine
MD Anderson Cancer Center, Houston, TX 77054
✉ krai@mdanderson.org

Martin Aryee, Ph.D.
Associate Professor, Dept of Data Science, Dana Farber Cancer Institute
Associate Professor, Dept of Biostatistics, Harvard TH Chan School of Public Health
Institute Member, Broad Institute of Harvard and MIT
Boston, MA 02215
✉ aryee.martin@mgh.harvard.edu

Alexander Meissner, Ph.D.
Director and Scientific member, Department of Genome Regulation,
Max Planck Institute for Molecular Genetics, Berlin, Germany
Berlin, Germany 14195

Additional references available upon request.