

Samirkumar B. Amin, MBBS, Ph.D.

Contact Information
 Yale University
 Department of Neurosurgery
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Education
Baylor College of Medicine, Houston, TX, USA
 Ph.D. – *Long non-coding RNA interactions in cancer* 08/2011 – 01/2017
 Quantitative & Computational Biosciences
 (prev. SCBMB) Graduate Program

Medical College & M S University of Baroda, Vadodara, Gujarat India
 Bachelor of Medicine, Bachelor of Surgery 11/1998 - 03/2005
 Accredited through The *Educational Commission for Foreign Medical Graduates* (ECFMG®), Philadelphia, PA, US 08/2006

Professional Experience
Associate Research Scientist 04/2023 – Present
 Department of Neurosurgery, Yale School of Medicine, New Haven, CT
 Advisor: Dr. Roel Verhaak, Ph.D.

- I have led a high-content CRISPR-Cas9 based imaging screen (HCS) to search & target cancer drivers in pediatric high-grade glioma. This project is in its completion phase with manuscript preparation underway.
- Contributed my expertise in the design and executing end-to-end data analysis workflows for two HCS-based projects in the lab.
- Contributed in analyzing single-cell and bulk whole-genome data for CSF-based liquid biopsy project at the *Ivy Brain Tumor Center*.

Postdoctoral Associate 01/2017 – 03/2023
 The Jackson Laboratory for Genomic Medicine, Farmington, CT, USA
 Advisor: Dr. Roel Verhaak, Ph.D.

- Led our study on comparative genomics of spontaneous canine and human glioma (Amin et al. 2020): Managed the entire project, collaborated with five veterinary schools and NCI on harmonizing data, integrated the largest cross-species whole-genome, exome, and transcriptomic data on canine and human glioma.
- Using comparative genomics approach, I am leading our ongoing high-throughput imaging based CRISPR-Cas9 screen to characterize cancer drivers in pediatric high-grade glioma: Designed guide RNAs for candidate genes in syntenic aneuploidies, led design for imaging screen with experimental biologists and core facility, implemented imaging-based post-knockout morphological profiling workflow to analyze 10M images (14 TB data) and subject lead targets for experimental validation.

Graduate Researcher 01/2012 - 01/2017
 Department of Genomic Medicine
 The University of Texas MD Anderson Cancer Center, Houston, TX USA
 Advisor: Dr. Lynda Chin, MD First 3.5 years
 Advisor: Dr. Roel Verhaak, Ph.D. Last 1.5 years

- Quantified expression of long non-coding RNAs (lncRNA) and provided lncRNA regulatory annotations as part of *Pan-Cancer Analysis of Whole Genomes* (PCAWG) of >2500 human cancers (Rheinbay et al. 2020).
- Performed integrative copy-number, expression, and network analysis to nominate candidate non-coding regulatory elements for functional validation using preclinical models for basic cancer biology and targeted drug discovery (Deribe et al. 2016; Carugo et al. 2019; Rondinelli et al. 2015).

Research Trainee 01/2008 - 06/2011
 Dana-Farber Cancer Institute, Boston, MA USA
 Mentor: Dr. Nikhil C. Munshi, MD, Medical Oncology
 Co-mentor: Dr. Cheng Li, PhD, Biostatistics & Computational Biology

- Using supervised machine learning approaches, filled an important gap in the early years of the precision medicine era by benchmarking the effectiveness of gene expression profiling-based biomarkers that were used to predict treatment response in myeloma (Amin et al. 2014).
- Contributed to an integrated, network-analysis based approaches to achieve better accuracy in predicting durable and, importantly, safer treatment options for patients with myeloma. (Yan et al. 2012; Wang et al. 2014)

Resident Physician 12/2005 - 11/2007
 Bhailal Amin General Hospital, Vadodara, Gujarat, India

- Managed care for patients with cancer under supervision of medical oncologists.

Teaching
 Experience

Certified Instructor for Software Carpentry 2019 – Present
 Software Carpentry is a non-profit organization of trained voluntary instructors for teaching structured workshops on computational programming to research staff in academia and industry, with a mission to foster an inclusive learning environment where people from diverse backgrounds have an open-access to interactive and collaborative training programs.

- **Programming in R and Linux**
The Jackson Laboratory & Univ. of Connecticut, Farmington, CT
 Audience: Graduate students and postdoctoral fellows.
- **Getting started with R**
Regeneron Pharmaceuticals, Tarrytown, NY
 Audience: Summer interns (high-school and undergraduate students).
- **Introduction to Unix Shell and git versioning**
Genentech, San Francisco, CA (Virtual)
 Audience: Research staff with a little or no prior experience in programming.

	Getting Started Guide to High-Performance Computing	2021 – Present
	Developed and continue to maintain a <i>Getting Started Guide to High-Performance Computing</i> , https://code.sbamin.com/hpc/ , for trainees with minimal experience in programming.	
Awards	Tumor Board Evolution Workshop Travel Award	2019
	Moffitt Physical Sciences Oncology Center, Tampa, FL	
	AACR Annual Meeting Scholar-in-Training Award	2018
	American Brain Tumor Association, Chicago, IL	
	Prof. John J. Trentin Award for Scholastic Excellence	2012
	Baylor College of Medicine, Houston, TX	
Funding Support	LindonLight Collective , \$ 343, 588	2023 – 2025
	Title: Targeting tumor-specific antigens in pediatric low-grade glioma. PI: Roel Verhaak, Ph.D. Role: Computational Biologist	
	Charlie Teo Foundation , \$ 275, 860	2020 – 2021
	Title: Targeting Regions of Converging Synteny and Loss of Heterozygosity in Pediatric and Canine Glioma. PI: Roel Verhaak, Ph.D. Role: Project Lead	
	Connecticut Children’s Medical Center , \$ 225, 000	2022 – 2023
	Title: High-throughput screening for genetic vulnerabilities in pediatric high-grade glioma. PI: Roel Verhaak, Ph.D. Role: Project Lead	
Publications	Total of 48 publications : 3 first-author, 29 co-authored, 1 preface, and 15 as part of the membership of large research consortia, e.g., TCGA, PCAWG, and GLASS. Complete list: https://www.ncbi.nlm.nih.gov/myncbi/samir.amin.2/bibliography/public/	
Work In Progress	Amin SB , Gujar A, Yi E, Kang W, Costa M, Sjogren G, et al. Poster Abstract 3106: Identifying drivers in the converging syntenic aneuploidies of spontaneous canine and pediatric high-grade glioma using imaging-based an arrayed CRISPR-Cas9 phenotypic screen. <i>Cancer Res</i> 2022;82:3106–3106. DOI: 10.1158/1538-7445.AM2022-3106.	
First Author Publications	Amin SB , Anderson KJ, Boudreau CE, Martinez-Ledesma E, ..., Heimberger AB, Levine JM, Verhaak RG. Comparative Molecular Life History of Spontaneous Canine and Human Gliomas. <i>Cancer Cell</i> 2020 Feb. PMID: 32049048. Featured as one of 12 key cancer datasets - along with TCGA and others - at the NCI Cancer Research Data Commons website, https://datacommons.cancer.gov/data	

Selected
Co-authored
Publications

- Amin SB**, Yip YK, Minvielle S, Avet-Loiseau H, Munshi NC et al. Gene expression profile alone is inadequate in predicting complete response in multiple myeloma. *Leukemia* 2014 AOP (Apr 15). PMID: 24732597.
- Amin SB**, Shah PK, Munshi NC, Li C, et al. The dChip survival analysis module for microarray data. *BMC Bioinformatics* 2011, 12(1):72. PMID: PMC3068974.
- Beck R, Tagal V, **Amin S**, Bakhoun SF, Maley C, Verhaak RGW, et al. Energetics of whole genome doubling and genomic instability. *Cancer Lett* 2025:217878. DOI: 10.1016/j.canlet.2025.217878
- Yi E, Gujar AD, Guthrie M, Kim H, Johnson KC, **Amin SB**, et al. Live-cell imaging shows uneven segregation of extrachromosomal DNA elements and transcriptionally active extrachromosomal DNA clusters in cancer. *Cancer Discov*. 2022 Feb. DOI: 10.1158/2159-8290.CD-21-1376
- Kocakavuk E, Anderson KJ, Varn FS, Johnson KC, **Amin SB**, Sulman EP, et al. Radiotherapy is associated with a deletion signature that contributes to poor outcomes in patients with cancer. *Nat Genet*. 2021 May; ; DOI: 10.1038/s41588-021-00874-3.
- Akdemir KC, Le VT, Kim JM, Killcoyne S, King DA, Li YP, Lian Y, Inoue A, **Amin SB**, ..., Dixon JR, Futreal PA., Process-specific somatic mutation distributions vary with three-dimensional genome structure. *Nat Genet*. 2020 Oct; DOI: 10.1038/s41588-020-0708-0.
- Rheinbay E, Nielsen MM, Abascal F, Tiao G, Hornshøj H, Hess JM, ..., **Amin SB**, ..., PCAWG Consortium. Analyses of Non-Coding Somatic Drivers in 2,658 Cancer Whole Genomes. *Nature* 2020 Feb. PMID: 32025015.
Executed pan-cancer expression profiling of lncRNAs and provided lncRNA regulatory annotations
- Kim H, Nguyen NP, Turner K, Wu S, Gujar AD, Luebeck J, Liu J, Deshpande V, Rajkumar U, Namburi S, **Amin SB**, Yi E, Menghi F, Schulte JH, Henssen AG, Chang HY, Beck CR, Mischel PS, Bafna V, Verhaak RGW. Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. *Nat Genet*. 2020 Sep. PMID: 32807987.
- Barthel F, Johnson KJ, ..., **Amin S**, ..., *GLASS Consortium*, Verhaak RGW. Longitudinal Molecular Trajectories of diffuse glioma in adults. *Nature*. 2019 Nov. PMID: 31748746.
- Adamia S, Abiatari I, **Amin S**, Fulciniti M, ..., Munshi N, Anderson K. The effects of MicroRNA deregulation on pre-RNA processing network in multiple myeloma. *Leukemia*. 2019 Jun. PMID: 31182781
- Carugo A, Minelli R, Sapio L, ..., **Amin S**, Srinivasan S, ..., Msaouel P, Tannir N, Draetta GF, Genovese G. p53 is a master regulator of proteostasis in SMARCB1-deficient rhabdoid tumors. *Cancer Cell* 2019 Feb. PMID: 30753823
- Genovese G, Carugo A, Tepper J, Robinson FS, Li L, Svelto M, Nezi L, Corti D, Minelli R, Pettazzoni P, Gutschner T, Wu CC, Seth S, Akdemir KC, Leo

E, **Amin SB**, Molin MD, Ying H, ..., Maitra A, Roberts CW, Wang H, Viale A, DePinho RA, Draetta GF, Chin L. Synthetic vulnerabilities of mesenchymal subpopulations in pancreatic cancer. *Nature*. 2017. PMID: 28178232

Barthel FP, Wei W, Tang M, Martinez-Ledesma E, Hu X, **Amin SB**, Akdemir KC, Seth S, Song X, Wang Q, Lichtenberg T, Hu J, Zhang J, Zheng S, Verhaak RG. Systematic analysis of telomere length and somatic alterations in 31 cancer types. *Nat Genet*. 2017 AOP (Jan 30). PMID: 28135248

Deribe YL, Shi Y, Rai K, **Amin SB**, Wu C, ..., Garraway L, Chin LY. Truncating PREX2 mutations activate its GEF activity and alter gene expression regulation in NRAS-mutant melanoma. *Proc Natl Acad Sci U S A*. 2016. PMID: 26884185.

Rondinelli B, Rosano D, Antonini E, Frenquelli M, Montanini L, Huang D, Segalla S, Yoshihara K, **Amin SB**, ..., Verhaak RG, Futreal PA, Di Croce L, Chin L, Cittaro D, Tonon G. Histone demethylase JARID1C inactivation triggers genomic instability in sporadic renal cancer. *J Clin Invest*. 2015, 125(12):4625. PMID:26551685.

Wang X, Yan Z, Fulciniti M, Li Y, Gkatzamanidou M, **Amin SB**, Li C et al. Transcription factor-pathway coexpression analysis reveals cooperation between SP1 and ESR1 on dysregulating cell cycle arrest in non-hyperdiploid multiple myeloma. *Leukemia* 2014,28(4):894-903. PMID: 23925045.

Tian Z, Zhao JJ, Tai YT, **Amin SB**, Chauhan D, Anderson KC et al. Investigational agent MLN9708/2238 targets tumor suppressor microRNA-33b in MM cells. *Blood* 2012 AOP (Sept 14). PMID: 22983447.

Yan Z, Shah PK, **Amin SB**, Li C, et al. Transcription factor-miRNA feed-forward loops account for a large proportion of transcriptome changes and identify regulators in human cancers. *Nucleic Acids Res*. 2012 AOP (May 29). PMID: 22645320.

Fulciniti M, **Amin SB**, Hideshima T, Anderson KC, Munshi NC, et al. Significant biological role of Sp1 transactivation in multiple myeloma. *Clin Cancer Res* 2011,17(20):6500. PMID: 21856768.

Book Chapters **Amin SB**. Machine Learning Approaches Pertinent to Glioma Classification in *Precision Molecular Pathology of Glioblastoma*. 1st edition. Springer Nature Switzerland AG. October 2020. ISBN: 978-3-030-69170-7

Yip WK, **Amin SB**, Li C. A Survey of Classification Techniques for Microarray Analysis in *Handbook of Statistical Bioinformatics*. 1st edition. Springer Science, New York, NY USA. May 2011. ISBN: 978-3-642-16344-9

Li C, **Amin S**. Analysis of Cancer Genome Alterations Using Single Nucleotide Polymorphism (SNP) Microarrays in *New developments in biostatistics and bioinformatics*. 1st edition. World Scientific Publishing Co., Singapore. April 2009. ISBN:981-283-743-4

Peer Reviewed Invited Talks	<p>Amin SB, Gujar A, Yi E, ..., Verhaak RG. High-content CRISPR-Cas9 optical screen to identify aneuploidy driver genes in pediatric high-grade glioma. <i>Cell Biology at Scale - Chan Zuckerberg Biohub Network</i>, West End Labs, New York, NY. Jul 31, 2025.</p> <p>Amin SB, Boudreau B, ..., Verhaak RG. Comparative molecular life history of spontaneous canine and human glioma. <i>23rd Annual Scientific Meeting of the Society for Neuro-Oncology</i>, JW Marriott Desert Ridge, Phoenix, AZ. Nov 22, 2019.</p> <p>Amin SB, Boudreau B, ..., Verhaak RG. Comparative molecular life history of spontaneous canine and human glioma. <i>23rd Annual Scientific Meeting of the Society for Neuro-Oncology</i>, Marriott Hotel, New Orleans, LA. Nov 16, 2018.</p> <p>Amin SB, Boudreau B, ..., Verhaak RG. Comparative molecular life history of spontaneous canine and human glioma. <i>Paws for a Cure Research Symposium</i>, Merck Research Laboratories, Boston, MA. Nov 12, 2018.</p> <p>Amin SB, Boudreau B, Martinez-Ledesma E, Kim H, Johnson K, Heimberger A, Levine J, Verhaak RG. Genomic profiling of canine glioma: Comparative analyses with respect to drivers of human glioma. <i>2nd Biannual Symposium of Comparative Brain Tumor Consortium</i>, National Institutes of Health, Bethesda, MD. Sep 18, 2017.</p> <p>Amin SB, Chang-Jiun W, Akdemir K, Rai K, Futreal A, Chin L. Profiling long intergenic non-coding RNA interactions in the cancer genome. <i>3rd Annual Scientific Symposium, The Cancer Genome Atlas Project</i>, National Institutes of Health, Bethesda, MD. May 13, 2014.</p> <p>Amin SB, Minvielle S, Hanlon B, Shah PK, Li C, Yi Li, Anderson KC, Avet-Loiseau H, Munshi NC. Gene Expression Profile Alone Is Inadequate In Predicting Complete Responses In Multiple Myeloma. <i>52nd Annual Meeting, American Society of Hematology</i>, Orlando, FL. December 6, 2010.</p>								
Mentoring	<table border="0" style="width: 100%;"> <tr> <td style="padding-right: 20px;">Yijun Dong, <i>Visiting MD-Ph.D. Student</i></td> <td style="text-align: right;">07/2024 – 09/2024</td> </tr> <tr> <td style="padding-right: 20px;">Emre Kocakavuk, <i>Visiting Research Fellow</i></td> <td style="text-align: right;">02/2019 – 04/2020</td> </tr> <tr> <td style="padding-right: 20px;">Margaret Chapman, <i>JAX Summer Student Program</i></td> <td style="text-align: right;">05/2017 – 08/2017</td> </tr> <tr> <td style="padding-right: 20px;">Ming "Tommy" Tang, <i>Postdoctoral fellow</i></td> <td style="text-align: right;">04/2015 – 12/2016</td> </tr> </table>	Yijun Dong, <i>Visiting MD-Ph.D. Student</i>	07/2024 – 09/2024	Emre Kocakavuk, <i>Visiting Research Fellow</i>	02/2019 – 04/2020	Margaret Chapman, <i>JAX Summer Student Program</i>	05/2017 – 08/2017	Ming "Tommy" Tang, <i>Postdoctoral fellow</i>	04/2015 – 12/2016
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Ming "Tommy" Tang, <i>Postdoctoral fellow</i>	04/2015 – 12/2016								
Professional Memberships	<p>Trainee membership in <i>American Association for Cancer Research</i> (2017–2025), <i>Society for NeuroOncology</i> (2018–2021), <i>American Society of Hematology</i> (2009–2011).</p>								
Professional Activities	<p>Grant Writing 2010 – Present</p> <ul style="list-style-type: none"> • 5P01CA155258-03, NIH NCI – <i>Integrative oncogenomics in multiple myeloma</i>. PI: Munshi NC et al.: Contributed writing for bioinformatics core section. • CTF-RV-20, Charlie Teo Foundation – <i>Targeting Regions of Converging Synteny and Loss of Heterozygosity in Pediatric and Canine Glioma</i>., PI: Verhaak RG. 								

- NIH NCI K99-R00 Pathway to Independence – *Comparative genomics of spontaneous canine and human pediatric glioma to characterize functional aneuploidy*: Unfunded (A0, A1, A0).

Ad-hoc Peer Reviewer 2011 – Present

Peer reviewed 60+ manuscripts: 12 for *Cancer Research*, 9 for *Bioinformatics*, 2 or more for *Genome Medicine*, *Nucleic Acid Research*, *PLOS Computational Biology*, *Blood Advances*, *PLOS ONE*, *PeerJ*.

Peer Reviewer 2018 – 2020

For The Jackson Laboratory *Summer Student Program*.

Scientific Judge 2019

Connecticut Science & Engineering Fair, Quinnipiac University.

Technical Skills	Programming languages: R, bash, git (daily) python and SQL (often) Computing: High-performance and cloud-based computing, large-scale data analysis, including GPU-based computing. Molecular biology: During graduate studies, performed cell culture, plasmid preparation, and PCR.
Version	4.4.web 01/2026. ■