ASHIR A. BORAH

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EDUCATION

University of California, San Francisco Sep 2022 – Present
Ph.D. Candidate, Biological and Medical Informatics *San Francisco, CA*

M.S., Biological and Medical Informatics — awarded en route to Ph.D. (advisor: Luke Gilbert) *Jun 2024*

- Advisors: Luke Gilbert (UCSF / Arc Institute) and Brian Hie (Stanford / Arc Institute).
- Research at the intersection of functional genomics, virology, and computational biology.

Dickinson College Aug 2015 – May 2019
Bachelor of Science, Mathematics and Computer Science *Carlisle, PA*

- *Magna Cum Laude*, Phi Beta Kappa. GPA: 3.89/4.00 (Major: 3.90/4.00).
- Senior research: *Computational analysis of phorbol 12-myristate 13-acetate (PMA) perturbation on human leukemia* (advisor: Michael Roberts).

RESEARCH EXPERIENCE

Arc Institute Jun 2023 – Present
Ph.D. Researcher (joint with UCSF) *Palo Alto, CA*

- Design and develop experimental and computational methods for functional genomics and virology.
- Build CRISPR-based screening and perturbation systems to study gene regulation, host–virus biology, and disease mechanisms.
- Develop assay platforms and analysis workflows for high-dimensional genomic datasets, including Perturb-seq.
- Build AI-enabled scientific tooling — LLM-based councils, research agents, APIs, and multi-agent workflows for literature synthesis, hypothesis generation, and experimental planning.

Broad Institute of MIT and Harvard Jul 2019 – Apr 2022
Computational Associate II (2021–2022); Computational Associate I (2019–2021) *Cambridge, MA*

Cancer Data Science — Cancer Dependency Map (DepMap) Project — advisor: James McFarland

- Led the computational effort to validate therapeutic genetic targets and identify their biomarkers.
- Developed strategies for discovering new targets from genome-scale CRISPR knockout screens, with a focus on GI cancers.
- Contributed to an open-source machine learning platform that models genetic-knockout dependency profiles from >100,000 genomic features.
- Modeled latent variables from genome-scale CRISPR-Cas9 screens to discover a new Integrator complex interaction.
- Analyzed RNAi and CRISPR screens as complementary data modalities for cancer-vulnerability discovery.

Dickinson College 2018 – 2019
Computational Research Assistant, Biochemistry and Molecular Biology *Carlisle, PA*

Advisor: Michael Roberts — topic: PMA perturbation in human leukemia

- Processed CRISPR knockout and overexpression genomic data on HL-60 leukemia cell lines.
- Identified differentially expressed genes from a compound perturbation that induced differentiation.
- Presented findings at the 2020 American Association for Cancer Research (AACR) annual meeting; subsequent students followed up on additional targets.

Uliza Sep 2017 – Dec 2017
Machine Learning Developer *Remote*

- Built ML-driven systems to support crowdsourced workflow automation.
- Helped set up core technical infrastructure — server management, database optimization, and disaster recovery.

PUBLICATIONS

Citation metrics (Google Scholar, Apr 2026): 1,125 citations — h-index 10 — i10-index 10.
Author names with **A.A. Borah** are mine.

Peer-reviewed publications

T.A. O'Loughlin, J.S. Stiles, P. Acharya, A. Arab, L. Goudy, R. Dai, **A.A. Borah**, *et al.* **mTORC1 activity suppresses ferroptosis through a SCARB1-dependent HDL-tocopherol uptake pathway**. *Molecular Cell* (2026). doi:10.1016/j.molcel.2026.02.019

H. Karner, T.C. Mittmann, V.W. Chen, **A.A. Borah**, A. Langen, H. Yousefi, L. Fish, *et al.* **Integrative analysis of mRNA stability regulation uncovers a metastasis-suppressive program in breast cancer**. *Science Advances* (2026). doi:10.1126/sciadv.aea9061

J. Gencel-Augusto, H. Li, L.C. Woerner, N. Tian, **A.A. Borah**, J.N. Myers, P. Ha, *et al.* **Human Papillomavirus does not fully inactivate p53 cellular activity in HNSCC**. *Head & Neck* (2026). doi:10.1002/hed.70085

P.C. Borck, I. Boyle, K. Jankovic, N. Bick, K. Foster, A.C. Lau, L.I. Parker-Burns, . . . , **A.A. Borah**, *et al.* **SKI complex loss renders 9p21.3-deleted or MSI-H cancers dependent on PELO**. *Nature* (2025). doi:10.1038/s41586-024-08509-3

L. Goudy, A. Ha, **A.A. Borah**, J.M. Umhoefer, L. Chow, C. Tran, A. Winters, *et al.* **Integrated epigenetic and genetic programming of primary human T cells**. *Nature Biotechnology* (2025). doi:10.1038/s41587-025-02856-w

M. Khoroshkin, D. Asarnow, S. Zhou, A. Navickas, A. Winters, J. Goudreau, . . . , **A.A. Borah**, *et al.* **A systematic search for RNA structural switches across the human transcriptome**. *Nature Methods* (2024). doi:10.1038/s41592-024-02335-1

S.J. Liu, C. Zou, J. Pak, A. Morse, D. Pang, T. Casey-Clyde, **A.A. Borah**, D. Wu, *et al.* **In vivo Perturb-seq of cancer and microenvironment cells dissects oncologic drivers and radiotherapy responses in glioblastoma**. *Genome Biology* (2024). doi:10.1186/s13059-024-03404-6

V.B. Venkadakrishnan, A.G. Presser, R. Singh, M.A. Booker, N.A. Traphagen, . . . , **A.A. Borah**, *et al.* **Lineage-specific canonical and non-canonical activity of EZH2 in advanced prostate cancer subtypes**. *Nature Communications* (2024). doi:10.1038/s41467-024-51156-5

L.D. Cervia, T. Shibue, **A.A. Borah**, B. Gaeta, L. He, L. Leung, N. Li, *et al.* **A ubiquitination cascade regulating the integrated stress response and survival in carcinomas**. *Cancer Discovery* (2023). doi:10.1158/2159-8290.CD-22-1230

J.M. Krill-Burger, J.M. Dempster, **A.A. Borah**, B.R. Paolella, D.E. Root, T.R. Golub, *et al.* **Partial gene suppression improves identification of cancer vulnerabilities when CRISPR-Cas9 knockout is pan-lethal**. *Genome Biology* (2023). doi:10.1186/s13059-023-03020-w

J. Pan, J.J. Kwon, J.A. Talamas, **A.A. Borah**, F. Vazquez, J.S. Boehm, *et al.* **Sparse dictionary learning recovers pleiotropy from human cell fitness screens**. *Cell Systems* (2022). doi:10.1016/j.cels.2022.01.005

S. Raghavan, P.S. Winter, A.W. Navia, H.L. Williams, A. DenAdel, K.E. Lowder, . . . , **A.A. Borah**, *et al.* **Microenvironment drives cell state, plasticity, and drug response in pancreatic cancer**. *Cell* (2021). doi:10.1016/j.cell.2021.11.017

N. van Wietmarschen, S. Sridharan, W.J. Nathan, A. Tubbs, E.M. Chan, . . . , **A.A. Borah**, *et al.* **Repeat expansions confer WRN dependence in microsatellite-unstable cancers**. *Nature* (2020). doi:10.1038/s41586-020-2769-8

Preprints

B.J. Woo, S. Sobti, J.M. Suh, H. Yousefi, K. Garcia, S. Zhou, **A.A. Borah**, *et al.* **Systematic identification of chromatin organizers as tuners of intratumoral heterogeneity**. *bioRxiv* (2026). doi:10.1101/2026.04.18.719392

Conference abstracts & posters

P.C. Borck, I. Boyle, K. Jankovic, N. Bick, K. Foster, A. Lau, L. Parker-Burns, . . . , **A.A. Borah**, *et al.* **Exploiting dysregulated ribosomal homeostasis in chromosome 9p21.3-deleted cancers and microsatellite-unstable cancers**. *Cancer Research 85 (8 Suppl. 2), Abstract SY14-03; AACR Annual Meeting* (2025).

E.M. Chan, P.C. Borck, N. Bick, K. Jankovic, I. Boyle, L. Parker-Burns, K. Foster, . . . , **A.A. Borah**, *et al.* **PELO is a synthetic lethal target in chromosome 9p21-deleted or MSI cancers**. *Cancer Research 84 (6 Suppl.), Abstract 3364; AACR Annual Meeting* (2024).

J.M. Krill-Burger, **A.A. Borah**, B.R. Paolella, J.M. McFarland, F. Vazquez. **Systematic methods to identify cancer vulnerabilities from genome-wide loss-of-function screens: an interactive framework for target discovery**. *Cancer Research 82 (12 Suppl.), Abstract 1897; AACR Annual Meeting* (2022).

L.D. Cervia, T. Shibue, B. Gaeta, **A.A. Borah**, L. Leung, N. Li, N. Dumont, *et al.* **A ubiquitination cascade regulates the integrated stress response and epithelial cancer survival**. *Cancer Research 81 (13 Suppl.), Abstract 1950; AACR Annual Meeting* (2021).

S. Raghavan, P.S. Winter, A.W. Navia, H.L. Williams, A. DenAdel, R.L. Kalekar, . . . , **A.A. Borah**, *et al.* **Transcriptional subtype-specific microenvironmental crosstalk and tumor cell plasticity in metastatic pancreatic cancer**. *Cancer Research 80 (22 Suppl.), Abstract PO-058; AACR Virtual Meeting II* (2020).

P.S. Winter, S. Raghavan, A.W. Navia, H.L. Williams, A. DenAdel, R.L. Kalekar, . . . , **A.A. Borah**, *et al.* **Subtype-specific microenvironmental crosstalk and tumor cell plasticity in metastatic pancreatic cancer**. *Cancer Research 80 (21 Suppl.), Abstract PR03; AACR Virtual Meeting II* (2020).

P.S. Winter, S. Raghavan, A.W. Navia, H. Williams, J. Galvez-Reyes, . . . , **A.A. Borah**, *et al.* **Matched metastatic pancreatic ductal adenocarcinoma biopsies and organoid models reveal tumor cell transcriptional plasticity and subtype-specific microenvironmental crosstalk**. *Cancer Research 80 (11 Suppl.), Abstract PR02; AACR Pancreatic Cancer Special Conference* (2020).

M. Roberts, L. Kageler, K. Bendinelli, S. Bonner, **A.A. Borah**, J. Forrester. **The role of EGR1 and AP1 in acute myeloid leukemia cell reprogramming toward cell cycle arrest and apoptosis**. *Cancer Research 80 (16 Suppl.), Abstract 4678; AACR Annual Meeting* (2020).

HONORS & AWARDS

Spot Award (×2), Broad Institute — for going above and beyond	2020, 2021
Phi Beta Kappa Honor Society	2019
Best Poster Award, All-College Science Symposium, Dickinson College	2019
Biology Department Summer Research Grant, Dickinson College	2018
Dana Research Assistantship, Dickinson College	2018
Pi Mu Epsilon — Mathematics National Honor Society	2018
Upsilon Pi Epsilon — Computer Science National Honor Society	2018
Richard Howland Memorial Scholarship — awarded to one student for excellence in Computer Science	2018
Jane Hill Prize in Computer Science — awarded to one first-year for excellence in CS	2016
Torchbearer Award, Bhumi — 6 recipients from a field of 8,000 volunteers	2015

TEACHING & MENTORING

Instructor — R Bootcamp for Biomedical Research 2022, 2023, 2024

University of California, San Francisco *San Francisco, CA*

- Brought the R bootcamp curriculum from the Broad Institute to UCSF and taught the course for three consecutive years to postdocs, clinicians, and graduate students.
- Adapted the original cancer-data-science curriculum to a broader biomedical audience; trained 250+ participants across the three offerings.

Course Creator and Teaching Assistant — Cancer Program R BootCamp 2019, 2021

Broad Institute of MIT and Harvard *Cambridge, MA*

- Designed and implemented the original curriculum to teach postdocs and graduate students the fundamentals of R for cancer data science.
- Trained ∼100 participants across the two offerings; received a Spot Award for voluntarily developing the course.

Research Mentor — UCSF PhD Rotation Students 2023 – Present

Gilbert Lab, UCSF / Arc Institute *San Francisco, CA*

- Mentored two UCSF PhD rotation students — one from the Bioinformatics (BMI) program and one from the Tetrad (basic biology) program — through introductory projects in functional genomics.

- Provided experimental and computational guidance and supported development of scientific writing, data analysis, and presentation skills.

Teaching Assistant — Mathematics and Computer Science 2016 – 2019
Dickinson College *Carlisle, PA*

- Courses: Introduction to Programming I, Introduction to Programming II, Data Structures.
- Facilitated lab sections, debugged student code, and graded assignments.

SERVICE

Ad-hoc Peer Reviewer
Nature Biotechnology

Co-chair — CodeRATS 2020 – 2021
Broad Institute of MIT and Harvard *Cambridge, MA*

- Co-led a community for early-career computational researchers.
- Held weekly office hours and facilitated periodic workshops on coding skills and tooling.

Volunteering Coordinator (North India) Jun 2014 – Jul 2015
Bhumi *New Delhi, India*

- Designed and implemented an after-school mathematics and science curriculum.
- Managed >100 volunteers and their projects, contributing 2,700 hours over a single year.

SKILLS & METHODS

Functional genomics: CRISPR screens (knockout, interference, activation), Perturb-seq, scRNA-seq, viral vector design, mammalian cell culture, cloning.

Single-cell analysis: Scanpy, Seurat, Cell Ranger, scVI, rapids-singlecell (GPU-accelerated workflows), MAGeCK.

Programming & ML: Python, R, PyTorch, JAX. Statistical modeling, dimensionality reduction, foundation models for DNA / RNA / protein.

AI tooling: LLM-based agents, multi-agent workflows, retrieval-augmented systems, LangChain, DSPy, scientific APIs, prompt engineering.

Languages (spoken): English (native), Hindi (professional), Assamese (conversational).