Shankara K. Anand

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ABOUT
I am a fourth year medical student at Boston University School of Medicine excited about oncology/critical care medicine and applying ML/AI to clinical practice. I have a masters from Stanford where I completed coursework in machine & deep learning and 4+ years of experience as a computational biologist at the Broad Institute of MIT & Harvard. My expertise includes single-cell genomics, multi-omic integration, and structural proteomics with an emphasis on algorithmic development.

EDUCATION

M.D. Candidate, Boston University, *Boston, MA* (exp.) 2024

M.S. Biomedical Informatics, Stanford University, *Stanford, CA* 2019

B.S. Chemical Engineering, Stanford University, *Stanford, CA* 2017

LICENSURE

USMLE Step 1 - Pass 04/06/2022

USMLE Step 2CK - 268 *(95th percentile)* 05/26/2023

RESEARCH

Associate Computational Biologist, Broad Institute of MIT & Harvard Aug. 2018 - Present
Supervised by Dr. Gad Getz & the Genotype Tissue Expression Experiment (GTEx)
- Led computational direction of pan-cancer, proteogenomic study (CPTAC)
- Mapped a single-nucleus, cross-tissue, transcriptome atlas of the human body (GTEx)
- Risk stratified Smoldering Multiple Myeloma patients with genomics (advised by Dr. Irene Ghobrial)

Researcher, Stanford Dept. of Bioengineering Jan. - June 2018
Supervised by Dr. Possu Huang
- Designed *de novo*, end-to-end (computational to wet-lab) proteins using Rosetta software
- Predicted ligand binding sites of proteins using deep learning frameworks (GitHub)

Scientific Intern, Novartis Summer 2017
Computer Aided Drug Discovery Team
- Developed machine learning framework for detecting pKa of in-house compounds
- Published work in *Journal of Chemical Information & Modeling*

Research Intern, Genentech Summer 2016
Early Stage Pharmaceutical Development
- Built computational pipeline for running large molecular dynamics simulations to investigate surfactant structure and antibody degradation

LEADERSHIP

Student Leader, BUSM Genetics Interest Group April 2021 - March 2022

Student Leader, BUSM in.Vision Tech x Medicine Group April 2021 - March 2022

STEM Tutor, Stanford Academic Resource Center Summer 2017

Dance Captain, Stanford Basmati Raas (Indian Dance) Sept. 2013 - June 2018

Resident Assistant, 2x years at Stanford Residential Education Sept. 2015 - June 2017

Program Coordinator, Stanford LGBT Community Resource Center Sept. 2015 - June 2017

VOLUNTEER

Child Life Volunteer, Boston Children's Hospital Oncology *(150 hrs)* Oct. 2018 - Feb. 2020

Fundraising Coordinator & Volunteer, Stanford Camp Kesem *(650 hrs)* April 2016 - July 2018

Reading Tutor, Stanford Ravenswood Reads *(120 hrs)* Spring 2016

AWARDS	**Eli Shapiro Academy**, BUSM Internal Medicine Honors	2023
	Scholar in Training Award, American Association of Cancer Research	2023
	Abstract Achievement Award, American Society of Hematology	2021
	Stanford Achievement Award, awarded to 10% of graduating class	2017
	Genentech Outstanding Student Award, selected Junior in Chemical Engineering	2016

SKILLS

Advanced: Python, R, PyTorch, TensorFlow, git

Basic: Matlab, LaTeX

SOFTWARE

Signature Analyzer: a fast, GPU enabled implementation of bayesian non-negative matrix factorization for extracting mutational and genomic expression signatures (GitHub).

CLUMPS-PTM: an algorithm for identifying 3D clusters of post-translational modifications (GitHub).

CLUMPS-2: an algorithm for identifying 3D clusters of somatic mutations (GitHub).

Mudi: python utilities for single-cell RNA-sequencing analyses (GitHub).

SITEFINDER: using deep learning to identify ligand site binding in proteins (Stanford CS231n) (GitHub).

PUBLICATIONS **Pre-Prints**

[1] Rouhana, J. M., Wang, J., Eraslan, G., **Anand, S.**, Hamel, A. R., Cole, B. et al. ECLIPSER: identifying causal cell types and genes for complex traits through single cell enrichment of e/sQTL-mapped genes in GWAS loci. bioRxiv (2021). doi: 10.1101/2021.11.24.469720

Peer-Reviewed Publications

[†] indicates co-first authorship

[‡] indicates co-second authorship

[1] Geffen, Y.[†], **Anand, S.**[†], Akiyama, Y.[†], Yaron, T.[†], Song, Y.[†], et al. Pan-Cancer Analysis of Post-Translational Modifications Reveals Shared Patterns of Protein Regulation. *Accepted to Cell*.

[2] Boiarsky, R., Haradhvala, N. J., Alberge, J. B., Sklavenitis-Pistofidis, R., Mouhieddine, T. H., Zavidij, O. et al. Single Cell Characterization of Myeloma and its Precursor Conditions Reveals Transcriptional Signatures of Early Tumorigenesis. **Nature Communications**, 13, 7040 (2022). doi: 10.1038/s41467-022-33944-z

[3] Sklavenitis-Pistofidis, R., Aranha, M. P., Redd, R. A., Baginska, J., Haradhvala, N. J., Hallisey, M., et al. Immune biomarkers of response to immunotherapy in patients with high-risk smoldering myeloma. **Cancer Cell**, 40(11), 1358-1373 (2022). doi: 10.1016/j.ccell.2022.10.017

[4] Yaron, T. M., Heaton, B. E., Levy, T. M., Johnson, J. L., Jordan, T. X., Cohen, B. M. et al. Host protein kinases required for SARS-CoV-2 nucleocapsid phosphorylation and viral replication. **Science Signaling**, 15(757) (2022). doi: 10.1126/scisignal.abm0808

[5] Roh, W., Geffen, Y., Cha, H., Miller, M., **Anand, S.**, Kim, J. et al. High-resolution profiling of lung adenocarcinoma identifies expression subtypes with specific biomarkers and clinically relevant vulnerabilities. **Cancer Research** (2022). doi: 10.1158/0008-5472.CAN-22-0432

[6] Knisbacher, B. A., Lin, Z., Hahn, C. K., Nadeu, F., Duran-Ferrer, M., Stevenson, K. E. et al. The CLL-1100 project: towards complete genomic characterization and improved prognostics for CLL. **Nature Genetics**, 1-11 (2022). doi: 10.1038/s41588-022-01140-w

[7] Bustoros, M.[†], **Anand, S.**[†], Sklavenitis-Pistofidis, R. et al. Genetic subtypes of smoldering multiple myeloma are associated with distinct pathogenic phenotypes and clinical outcomes. **Nature Communications**, 13, 3449 (2022). doi: 10.1038/s41467-022-30694-w (GitHub)

[8] Eraslan, G.[†], Drokhlyansky, E.[†], **Anand, S.**[‡], Fiskin, E.[‡], Subramanian, A.[‡], Sylper, M.[‡], Wang, J.[‡] et al. Single-nucleus cross-tissue molecular reference maps toward understanding disease gene

function. **Science**, 376(6594) (2022). doi: 10.1126/science.abl4290

[9] Beauchamp, E. M., Leventhal, M., Bernard, E., Hoppe, E. R., Todisco, G., Creignou, M. et al. ZBTB33 is mutated in clonal hematopoiesis and myelodysplastic syndromes and impacts RNA splicing. **Blood Cancer Discovery**, 2(5), 500-517 (2021). doi: 10.1158/2643-3230.BCD-20-0224

[10] Satpathy, S., Krug, K., Beltran, P. M. J., Savage, S. R., Petralia, F., Kumar-Sinha, C. et al. A proteogenomic portrait of lung squamous cell carcinoma. **Cell**, 184(16), 4348-4371 (2021). doi: 10.1016/j.cell.2021.07.016

[11] de Goede, O. M., Nachun, D. C., Ferraro, N. M., Gloudemans, M. J., Rao, A. S., Smail, C. et al. Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. **Cell**, 184(10), 2633-2648 (2021). doi: 10.1016/j.cell.2021.03.050

[12] Jiang, L., Wang, M., Lin, S., Jian, R., Li, X., Chan, J. et al. A quantitative proteome map of the human body. **Cell**, 183(1), 269-283 (2020). doi: 10.1016/j.cell.2020.08.036

[13] Ferraro, N. M., Strober, B. J., Einson, J., Abell, N. S., Aguet, F., Barbeira, A. N. et al. Transcriptomic signatures across human tissues identify functional rare genetic variation. **Science**, 369(6509) (2020). doi: 10.1126/science.aaz5900

[14] GTEx Consortium. The GTEx Consortium atlas of genetic regulatory effects across human tissues. **Science**, 369(6509), 1318-1330 (2020). doi: 10.1126/science.aaz1776

[15] Bustoros, M., Sklavenitis-Pistofidis, R., Park, J., Redd, R., Zhitomirsky, B., Dunford, A. J. et al. Genomic profiling of smoldering multiple myeloma identifies patients at a high risk of disease progression. **Journal of Clinical Oncology**, 38(21), 2380 (2020). doi: 10.1200/JCO.20.00437

[16] Taylor-Weiner, A., Aguet, F., Haradhvala, N. J., Gosai, S., **Anand, S.**, Kim, J. et al. Scaling computational genomics to millions of individuals with GPUs. **Genome Biology**, 20(1), 1-5 (2019). doi: 10.1186/s13059-019-1836-7

[17] Lu, Y., **Anand, S.**, Shirley, W., Gedeck, P., Kelley, B. P., Skolnik, S. et al. Prediction of p K a using machine learning methods with rooted topological torsion fingerprints: application to aliphatic amines. **Journal of Chemical Information and Modeling**, 59(11), 4706-4719 (2019). doi: 10.1021/acs.jcim.9b00498

[18] **Anand, S.**, Kalesinskas, L., Smail, C., & Tanigawa, Y. SNPs2ChIP: Latent Factors of ChIP-seq to infer functions of non-coding SNPs. **Proceedings of the Pacific Symposium** (pp. 184-195) (2018). doi: 10.1142/9789813279827_0017

PRESENTATION **Talks**

[1] Roh, W., Geffen, Y., Miller, M., **Anand, S.**, Kim, J., Heiman, D. et al. Identification and proteogenomic characterization of novel lung adenocarcinoma subtypes with therapeutic relevance. **American Association of Cancer Research (AACR)**, 82(12_Supplement), 2151-2151 (2022). doi: 10.1158/1538-7445.AM2022-2151

[2] Kubler, K., Nardone, A., **Anand, S.**, Gorvich, D., Droog, M., Hermida-Prado, F. et al. Abstract GS2-09: Tamoxifen instigates uterine cancer development by activating PI3K signaling and supersedes PIK3CA driver mutations. **San Antonio Breast Cancer Symposium (SABCS)**, 82(4_Supplement) (2021). doi: 10.1158/1538-7445.SABCS21-GS2-09

[3] Sklavenitis-Pistofidis, R., Dutta, A. K., Ujwary, S., Redd, R. A., Savell, A., Fléchon, L. et al. Single-Cell RNA-Sequencing Identifies Immune Biomarkers of Response to Immunotherapy in Patients with High-Risk Smoldering Myeloma. **American Society of Hematology (ASH)**, 138, 330 (2021). doi: 10.1182/blood-2021-147623

[4] **Anand, S.**[†], Bustoros, M.[†], Sklavenitis-Pistofidis, R., Redd, R. A., Boyle, E. M., Tai, Y. T. et al. Genomic Profiling of Smoldering Multiple Myeloma Classifies Molecular Groups with Distinct Pathogenic Phenotypes and Clinical Outcomes. **American Society of Hematology (ASH)**, 138, 723 (2021).

[5] **Anand, S.** "Genomic profiling of smoldering myeloma identifies high- and low- risk patients | ASH

2021." **The Video Journal of Hematological Oncology**, Dec. 12, 2021. Interviews: Part 1. Part 2.

[6] Geffen, Y.[†], **Anand, S.[†]**, Akiyama, Y.[†], Yaron, T. M., Kerelsky, A., Johnson, J. L., ... & Oncogenic Drivers and Pathways Group, Clinical Proteomic Tumor Analysis Consortium (CPTAC). Patterns and regulation of post translational modifications in cancer. **American Association of Cancer Research (AACR)**, 81(13_Supplement), 16-16. doi: 10.1158/1538-7445.AM2021-16

Posters & Abstracts

[1] **Anand, S.**, Geffen, Y., Akiyama, Y., Aguet, F., Getz, G. *CLUMPS-PTM*: Spatial Clustering of Post-Translational Modifications Across Cancer Types. **American Association of Cancer Research (AACR)**, 83(7_Supplement), 3132-3132 (2023). doi: 10.1158/1538-7445.AM2023-3132

[2] Li, G. X., Hsiao, Y., Chen, L., Mannan, R., Zhang, Y., Petralia, F., et al. Comprehensive proteogenomic characterization of rare kidney tumors. **American Association of Cancer Research (AACR)**, 83(7_Supplement), 3127-3127 (2023). doi: 10.1158/1538-7445.AM2023-3127

[3] Boiarsky, R., Haradhvala, N., Sklavenitis-Pistofidis, R., Mouhieddine, T. H., Alberge, J. B., Zavidij, O. et al. Single Cell Characterization of Myeloma and its Precursor Conditions Reveals Transcriptional Signatures of Early Tumorigenesis. **American Society of Hematology (ASH)**, 138, 2219 (2021). doi: 10.1182/blood-2021-150889

[4] Akiyama, Y., Geffen, Y., **Anand, S.**, Yaron, T., Johnson, J. L., Huntsman, E. et al. Pan-cancer proteogenomic analysis reveals functional mechanisms underlying DNA repair deficiencies. **American Association of Cancer Research (AACR)**, 82(12_Supplement), 794-794 (2022). doi: 10.1158/1538-7445.AM2022-794

[5] **Anand, S.**, Bustoros, M., Aguet, F., Sklavenitis-Pistofidis, R., Redd, R., Zhitomirsky, B. et al. Genomic profiling of smoldering multiple myeloma classifies distinct molecular groups. **American Association of Cancer Research (AACR)**, 81(13_Supplement), 2240-2240 (2021). doi: 10.1158/1538-7445.AM2021-2240

[6] **Anand, S.**, Aguet, F., Taylor-Weiner, A., et al. Signature Analyzer: scaling Bayesian NMF to millions of individuals with GPUs. **Broad Institute of MIT & Harvard Retreat**, (2019). GitHub.

INTERESTS

Rass/Garba (Indian) dance: 5+ years of dancing and choreographing at cultural events (ex. Stanford Holi), national competitions, and family weddings.

Music: 15+ years of classical violin training, performed with Stanford Symphony Orchestra, chamber music groups, and musical theater pit orchestras; also enjoy guitar & ukulele.

Dogs: my wife and I have a 3 year old Mudi dog, Hazel, that we do trick training, frisbee catching, and agility with. She comes with us back-country skiing and watches over us when we climb outdoors.

Ski Mountaineering: ask me about the glacier we climbed up and skied down in the Selkirk Mountains of British Columbia!

Rock Climbing: we love indoor & outdoor lead climbing + finding new routes along the Pacific Coast.