# Shankara K. Anand

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**ABOUT**

I am a computational biologist and rising PGY-2 in internal medicine in Stanford's Translational Investigator Pathway for Hematology/Oncology. I am interested in plasma cell dyscrasias, amyloidosis, precision oncology, and early cancer detection. I have a Masters in machine/deep learning for medical applications and 5+ years of genomics expertise from the Broad Institute at MIT & Harvard. My research includes single-cell genomics, multi-omics, structural proteomics, and algorithm development.

**CLINICAL**

**Resident Physician**, Internal Medicine, Stanford Health Care, *Stanford, CA*     2024 - present
- Translational Investigator Pathway (Hematology/Oncology)
- IM Health Equity, Advocacy, and Research (HEARS) Pathway

**EDUCATION**

**M.D.** (Cum Laude), Boston University School of Medicine, *Boston, MA*     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     05/26/2023
**USMLE Step 3** - 241     10/11/2024

**RESEARCH**

**Researcher**, Boston University School of Medicine     2023 - 2024
Supervised by Dr. Vaishali Sanchorawala & Dr. Ashish Verma
- Risk stratification & prediction of all-cause mortality and progression to ESKD in AL Amyloidosis
- Published in *American Journal of Hematology*

**Associate Computational Biologist**, Broad Institute of MIT & Harvard     2018 - 2023
Supervised by Dr. Gad Getz & the Genotype Tissue Expression Experiment (GTEx)
- Co-led pan-cancer, proteogenomic study, published in *Cell* (CPTAC)
- Mapped single-nucleus, cross-tissue atlas of the human body, published in *Science* (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 and tested *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 in *Journal of Chemical Information & Modeling*

**Research Intern**, Genentech     Summer 2016
Early Stage Pharmaceutical Development
- Built molecular dynamics simulation pipeline to investigate antibody degradation

**LEADERSHIP**

**Internal Medicine Student Chief**, BUSM Internal Medicine Clerkship     June 2023 - May 2024

**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

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| | **Resident Assistant**, 2x years at Stanford Residential Education | Sept. 2015 - June 2017 |
| | **Program Coordinator**, Stanford LGBT Community Resource Center | Sept. 2015 - June 2017 |

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| VOLUNTEER | **Child Life Volunteer**, Boston Children's Hospital Oncology (*150 hrs*) | Oct. 2018 - Feb. 2020 |
| | **Fundraising Coordinator & Volunteer**, Stanford Camp Kesem (*500 hrs*) | April 2016 - July 2018 |
| | **Reading Tutor**, Stanford Ravenswood Reads (*120 hrs*) | Spring 2016 |

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| AWARDS | **International Society of Amyloidosis**, Junior Investigator Travel Award | 2024 |
| | **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 / Under Review**

[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] Kołodziejczak-Guglas, I., Simões, R. L., de Souza Santos, E., Demicco, E. G., Segura, R. N. L., Ma, W., et al. Proteomic-based stemness score measures oncogenic dedifferentiation and enables the identification of druggable targets. **Cell Genomics**, (2025). doi: 10.1016/j.xgen.2025.100851

[2] Rodrigues, F. M., Terekhanova, N. V., Imbach, K. J., Clauser, K. R., Selvan, M. E., Mendizabal, I., et al. Precision proteogenomics reveals pan-cancer impact of germline variants. **Cell**, 188(9), 2312-2335, (2025). doi: 10.1016/j.cell.2025.03.026

[3] **Anand, S.**[†], O'Neill-Dee, M., Sanchorawala, V., Verma, A. Light-chain (AL) amyloidosis for nephrologists - treatment standard. **Nephrology Dialysis Transplantation**, 40(1), 34-47, (2025). doi: 10.1093/ndt/gfae224

[4] **Anand, S.**[†], Staron, A., Mendelson, L. M., Joshi, T., Burke, N., Sanchorawala, V., Verma, A. Machine-learning based subgroups of AL amyloidosis and cumulative incidence of mortality and end stage kidney disease. **American Journal of Hematology**, (2024). doi: 10.1002/ajh.27472

[5] **Anand, S.**[†], Verma, A., Sanchorawala, V. Systemic Amyloidosis and Kidney Transplantation: An Update. **Seminars in Nephrology**, (2024). doi: 10.1016/j.semnephrol.2024.151496

[6] Li, G. X., Chen, L., Hsiao, Y., Mannan, R., Zhang, Y., Luo, J., et al. Comprehensive proteogenomic characterization of rare kidney tumors. **Cell Reports Medicine**, 5(5), (2024). doi: 10.1016/j.xcrm.2024.101

[7] 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. **Cell**, 186, 1-24 (2023). doi: 10.1016/j.cell.2023.07.013

[8] Li, Y., Porta-Pardo, E., Tokheim, C., Bailey, M.H., Yaron, T.M., Stathias, V., Geffen, Y., Imbach, K.J., Cao, S., **Anand, S.**, Akiyama, Y., et al. Pan-cancer proteogenomics connects oncogenic drivers to functional states. **Cell**, 186, 1–24 (2023). doi: 10.1016/j.cell.2023.07.014

[9] Li, Y., Dou, Y., Leprevost, F. D. V., Geffen, Y., Calinawan, A. P., Aguet, F., Akiyama, Y., **Anand, S.**, et al. Proteogenomic data and resources for pan-cancer analysis. **Cancer Cell**, 41(8), 1397-1406 (2023). doi: 10.1016/j.ccell.2023.06.009

[10] 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

[11] 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

[12] 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

[13] 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

[14] 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

[15] 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)

[16] 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

[17] 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

[18] 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

[19] 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

[20] 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

[21] 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

[22] GTEx Consortium. The GTEx Consortium atlas of genetic regulatory effects across human tissues.

**Science**, 369(6509), 1318-1330 (2020). doi: 10.1126/science.aaz1776

[23] 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

[24] 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

[25] 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

[26] **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

**Peer-Reviewed Book Chapters**

[1] **Anand, S.**, Verma, A. (2023). *Artificial Intelligence in Nephrology*. In C. Krittanawong (Ed.), Artificial Intelligence in Clinical Practice: How AI Technologies Impact Medical Research and Clinics (First Edition). New York City: Elsevier.

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.**, Staron, A., Mendelson, L. M., Joshi, T., Burke, N. J., Sanchorawala, V., Verma, A. Machine-Learning Based Subgroups of AL Amyloidosis and Cumulative Incidence of Mortality and End Stage Kidney Disease. **International Symposium on Amyloidosis**, (2024).

[2] **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

[3] 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

[4] 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

[5] 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

[6] **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

[7] **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.

HOBBIES    **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.

**Dog:** My wife and I have a 4 year old Mudi dog, Hazel, who we do agility and frisbee catching with.

**Ski Mountaineering:** Ask me about the glacier we climbed and skied down in the Selkirk Mountains!

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