

Shankara K. Anand



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ABOUT	I am a physician scientist, Hematology/Oncology fellow, and computational biologist in Stanford's Translational Investigator Pathway. I am interested in plasma cell dyscrasias, amyloidosis, precision oncology, and early cancer detection. I have a Master's in machine/deep learning for medical applications and 5+ years of genomics expertise from the Broad Institute of MIT & Harvard. My research includes single-cell genomics, multi-omics, structural proteomics, and algorithm development.	
CLINICAL	Fellow , Hematology/Oncology, Stanford Health Care, <i>Stanford, CA</i> • Translational Investigator Pathway	2026 - present
	Resident Physician , Internal Medicine, Stanford Health Care, <i>Stanford, CA</i> • IM Health Equity, Advocacy, and Research (HEARS) Pathway	2024 - 2026
EDUCATION	M.D. (Cum Laude), Boston University School of Medicine, <i>Boston, MA</i>	2024
	M.S. Biomedical Informatics , Stanford University, <i>Stanford, CA</i>	2019
	B.S. Chemical Engineering , Stanford University, <i>Stanford, CA</i>	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 Supervised by Dr. Vaishali Sanchorawala & Dr. Ashish Verma • Risk stratification & prediction of all-cause mortality and progression to ESKD in AL Amyloidosis • Published in <i>American Journal of Hematology</i>	2023 - 2024
	Associate Computational Biologist , Broad Institute of MIT & Harvard Supervised by Dr. Gad Getz & the Genotype Tissue Expression (GTEx) Consortium • Co-led pan-cancer, proteogenomic study, published in <i>Cell</i> (CPTAC) • Mapped single-nucleus, cross-tissue atlas of the human body, published in <i>Science</i> (GTEx) • Risk stratified Smoldering Multiple Myeloma patients with genomics (advised by Dr. Irene Ghobrial)	2018 - 2023
	Researcher , Stanford Dept. of Bioengineering Supervised by Dr. Possu Huang • Designed and tested <i>de novo</i> , end-to-end (computational to wet-lab) proteins using Rosetta software • Predicted ligand binding sites of proteins using deep learning frameworks (GitHub)	Jan. - June 2018
	Scientific Intern , Novartis Computer Aided Drug Discovery Team • Developed machine learning framework for detecting pKa of in-house compounds • Published in <i>Journal of Chemical Information & Modeling</i>	Summer 2017
	Research Intern , Genentech Early Stage Pharmaceutical Development • Built molecular dynamics simulation pipeline to investigate antibody degradation	Summer 2016
	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
	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 (<i>150 hrs</i>)	Oct. 2018 - Feb. 2020
	Fundraising Coordinator & Volunteer , Stanford Camp Kesem (<i>500 hrs</i>)	April 2016 - July 2018
	Reading Tutor , Stanford Ravenswood Reads (<i>120 hrs</i>)	Spring 2016
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] Kübler, K., Nardone, A., Anand, S. , Gurevich, D., Gao, J., Droog, M., et al. Tamoxifen induces PI3K activation in uterine cancer. Nature Genetics , 1-11(2025). doi: 10.1038/s41588-025-02308-w	
	[2] Satpathy, S., Clark, N. M., Chen, Y. J., Hosseini, N., Chang, Y. H., Hsiao, Y., et al. Integrative analysis of lung adenocarcinoma across diverse ethnicities and exposures. Cancer Cell , (2025). doi: 10.1016/j.ccell.2025.07.011	
	[3] 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	
	[4] 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	

- [5] **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](https://doi.org/10.1093/ndt/gfae224)
- [6] **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](https://doi.org/10.1002/ajh.27472)
- [7] **Anand, S.[†]**, Verma, A., Sanchorawala, V. Systemic Amyloidosis and Kidney Transplantation: An Update. **Seminars in Nephrology**, (2024). doi: [10.1016/j.semnephrol.2024.151496](https://doi.org/10.1016/j.semnephrol.2024.151496)
- [8] 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.2024.101496](https://doi.org/10.1016/j.xcrm.2024.101496)
- [9] 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](https://doi.org/10.1016/j.cell.2023.07.013)
- [10] 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](https://doi.org/10.1016/j.cell.2023.07.014)
- [11] 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](https://doi.org/10.1016/j.ccell.2023.06.009)
- [12] 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](https://doi.org/10.1038/s41467-022-33944-z)
- [13] 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](https://doi.org/10.1016/j.ccell.2022.10.017)
- [14] 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](https://doi.org/10.1126/scisignal.abm0808)
- [15] 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](https://doi.org/10.1158/0008-5472.CAN-22-0432)
- [16] 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](https://doi.org/10.1038/s41588-022-01140-w)
- [17] 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](https://doi.org/10.1038/s41467-022-30694-w) (GitHub)
- [18] Eraslan, G.[†], Drokhyansky, E.[†], **Anand, S.[‡]**, Fiskin, E.[‡], Subramanian, A.[‡], Slyper, 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](https://doi.org/10.1126/science.abl4290)
- [19] 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](https://doi.org/10.1158/2643-3230.BCD-20-0224)
- [20] 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](https://doi.org/10.1016/j.cell.2021.07.016)
- [21] 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](https://doi.org/10.1016/j.cell.2021.03.050)
- [22] 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](https://doi.org/10.1016/j.cell.2020.08.036)
- [23] 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](https://doi.org/10.1126/science.aaz5900)
- [24] GTEx Consortium. The GTEx Consortium atlas of genetic regulatory effects across human tissues. **Science**, 369(6509), 1318-1330 (2020). doi: [10.1126/science.aaz1776](https://doi.org/10.1126/science.aaz1776)
- [25] 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](https://doi.org/10.1200/JCO.20.00437)
- [26] 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](https://doi.org/10.1186/s13059-019-1836-7)
- [27] Lu, Y., **Anand, S.**, Shirley, W., Gedeck, P., Kelley, B. P., Skolnik, S. et al. Prediction of pK_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](https://doi.org/10.1021/acs.jcim.9b00498)
- [28] **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](https://doi.org/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](https://doi.org/10.1158/1538-7445.AM2022-2151)
- [2] Kubler, K., Nardone, A., **Anand, S.**, Gurevich, 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](https://doi.org/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](https://doi.org/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**

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 6 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.