Keagan Moo 425-445-0455 keagan@moomail.us

Education	University of Michigan (UM) (2021 – Present) PhD in Bioinformatics Omics and Machine Learning Concentration
	University of Washington (UW) (2013 – 2017) Bachelors of Science in Bioengineering Synthetic and Computational Biology Focus
Work	 Parker Lab (University of Michigan) (2022 – Present) Graduate Student Research Assistant Performed single nucleus multi-modal (RNA and ATAC data) research in human skeletal muscle studying the effects of aging using a diverse suite of modeling and enrichment testing tools Built and used nextflow data processing pipelines to ensure data quality according to lab standards
	 Khor Lab (Benaroya Research Institute) (2017 – 2021) Research Technician Managed in vitro and in vivo experiments for translational research investigating the effects of DYRK1A expression on T-cell differentiation and function in relation to the pathology of Down Syndrome Developed an R pipeline for differential aging analysis and applied it to an immunology focused CyTOF panel on whole PBMCs comparing Down Syndrome, Type 1 Diabetic, and Typical Control subjects Produced an R pipeline for RNASeq and differential co-expression analysis for both differential gene and exon expression in accordance with the BRI bioinformatics core standards
	 Kyung Hyuk Kim Lab (University of Washington) (2015 – 2017) Undergraduate Research Assistant Built a machine learning tool to predict the efficacy of combined cancer drug treatments for the AstraZeneca DREAM challenge Characterized genetic circuit dynamics using a Sequential Monte Carlo Bayesian learning tool written in python to inform decisions about circuit design, transfection priority, and environmental impact
	 Novo Nordisk (Summer of 2014 and 2016) Bioinformatics Intern Worked with the bioinformatics team to incorporate differential exon analysis tools to an existing RNASeq analysis pipeline Performed differential expression analysis on activated T-cells from individuals with autoimmune conditions with a focus on T1D Used a combination of ImageJ and R to build an automated tool for annotating histology images for invaded islet cells in the pancreas

Skills	R, Python, UNIX Scripting, SLURM job management, Nextflow, Torch, DESeq2, MAST, ARIMA, FlowJo, Prism, Matlab, ImageJ, Java, Perl, SQL, Shiny, Microsoft Office
Awards	Honors Undergraduate Scholar Award Scholarship (UW 2013) Dean's List (UW, 2015 – 2017) Reviewers Choice Abstract ASHG (2023)
Publications	Published
	Lambert, K., Moo, K. G. , Arnett, A., Goel, G., Hu, A., Flynn, K. J., Speake, C., Wiedeman, A. E., Gersuk, V. H., Linsley, P. S., Greenbaum, C. J., Long, S. A., Partridge, R., Buckner, J. H., & Khor, B. (2022). Deep immune phenotyping reveals similarities between aging, Down syndrome, and autoimmunity . <i>Science translational medicine</i> , 14(627), eabi4888. https://doi.org/10.1126/scitranslmed.abi4888
	Arnett, A., Moo, K. G. , Flynn, K. J., Sundberg, T. B., Johannessen, L., Shamji, A. F., Gray, N. S., Decker, T., Zheng, Y., Gersuk, V. H., Rahman, Z. S., Levy, D. E., Marié, I. J., Linsley, P. S., Xavier, R. J., & Khor, B. (2021). The Cyclin-Dependent Kinase 8 (CDK8) Inhibitor DCA Promotes a Tolerogenic Chemical Immunophenotype in CD4+ T Cells via a Novel CDK8-GATA3-FOXP3 Pathway . <i>Molecular and</i> <i>cellular biology</i> , 41(9), e0008521. https://doi.org/10.1128/MCB.00085-21
	Bolouri, H., Speake, C., Skibinski, D., Long, S. A., Hocking, A. M., Campbell, D. J., Hamerman, J. A., Malhotra, U., Buckner, J. H., & Benaroya Research Institute COVID-19 Research Team (2021). The COVID-19 immune landscape is dynamically and reversibly correlated with disease severity. <i>The Journal of clinical investigation</i> , 131(3), e143648. https://doi.org/10.1172/JCI143648
Presentations	Wilske Seminar DYRK1A Regulates Th17/Treg Differentiation (2020)
	Effects of DYRK1A Overexpression on T-Cell Differentiation and Function (2019)
	BRI Translational Meeting Immune Landscape of Down Syndrome: First glimpses at BRI (February 2020)
	American Society for Human Genetics (ASHG) Poster: Widespread age-associated changes in the chromatin architecture of skeletal muscle cell types (2022 & 2023)
	American Diabetes Association (ADA) Platform Talk: Widespread age-associated changes in the chromatin architecture of skeletal muscle cell types (2024)