

Sasha Chernenkoff

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Education

Master of Science, Specialization in Bioinformatics · Cumming School of Medicine, University of Calgary, Canada · *Expected February 2027*

GPA: 4.0/4.0

Thesis: Transfer learning reveals post-transcriptional sequence determinants of protein abundance

Areas of interest: machine learning, representation learning, computational genomics, statistical genetics

Bachelor of Science, Honours in Chemistry · Dietrich School of Arts and Sciences, University of Pittsburgh, USA

GPA: 4.0/4.0

Thesis: Selective inhibition of histone lysine demethylases using sterically modified inhibitors

Experience

Research Associate · University of Calgary, Canada

August 2023 - Present

- Fine-tuning a genomic foundation model to predict protein abundance from DNA sequence, and using in silico mutagenesis to study what the retargeted model learns (PASTL)
- Developing a categorical VAE that compresses genome-wide genotypes into low-dimensional representations for SNP heritability estimation (HERL)
- Building a multi-GPU training system with LoRA adapters and custom loss functions for personalized gene expression prediction from diploid genomes

R&D Scientist II / I · PerkinElmer Genomics

June 2020 - July 2023

Developed second-tier biochemical diagnostic tests for newborn screening programs: LC-MS/MS biomarker panel for MPS I & II; Western blot CRIM-status assay for Pompe disease

Undergraduate Research Associate · University of Pittsburgh, USA

September 2018 - June 2020

Synthesized small-molecule inhibitors of enzymes involved in transcriptional regulation and used mutagenesis to generate enzyme variants for evaluating inhibitor selectivity and binding mechanisms

Publications

Chernenkoff, S., Enoma, D., Weeraman, J. & Long, Q. Transfer learning reveals post-transcriptional sequence determinants of protein abundance. *In preparation* (2026).

Kemogne, A., Weeraman, J., Wang, D., Enoma, D., Li, C., Sridharan, G., Chernenkoff, S., Chekouo, T., Zhang, Q. & Long, Q. Genomic variational autoencoder enables stable representation learning in high-dimensional genomic data with moderate sample sizes. *Under review* (2026).

Kuwik, J., Hinkelman, K., Waldman, M., Stepler, K. E., Wagner, S., Arora, S., Chernenkoff, S., Cabalteja, C., Sidoli, S., Robinson, R. A. S. & Islam, K. Activity guided azide-methyllysine photo-trapping for substrate profiling of lysine demethylases. *J. Am. Chem. Soc.* **145**, 21066-21076 (2023).

Abstracts

Donti, T., Smith, S., Chernenkoff, S., Ellgass, M. & Hegde, M. P012: Measuring non-reducing terminal glycosaminoglycan fragments increases specificity and differentiates mucopolysaccharidosis type I (MPS I) from mucopolysaccharidosis type II (MPS II). *Genet. Med. Open* **1**, 100022 (2023).

Poster Presentations

Chernenkoff, S., Enoma, D., Weeraman, J. & Long, Q. Transfer learning reveals post-transcriptional sequence determinants of protein abundance. *ASHG Annual Meeting*, Montreal, QC (2026).

Chernenkoff, S., Zhang, Q. & Long, Q. Variant annotation for low-prevalent disorders empowered by transfer-learning. *ACHRI Research Retreat*, Banff, AB (2023).

Smith, S. E., Gelb, M. W., Herbst, Z. M., Dellagatta, J. N., Chernenkoff, S., Donti, T. & Khaledi, H. Measurement of non-reducing terminal glycosaminoglycan fragment increases specificity of second-tier testing for mucopolysaccharidosis type I (MPS I). *APHL Newborn Screening Symposium*, Tacoma, WA (2022).

Awards & Scholarships

ACHRI Graduate Scholarship

September 2026

Canada Graduate Scholarships - Master's Program (CIHR)

April 2024

Phillips Medal

February 2020

American Chemical Society Undergraduate Award in Organic Chemistry

October 2019

Skills

Languages & ML: Python · PyTorch · PyTorch DDP · LoRA/PEFT · pandas · NumPy · SciPy · scikit-learn · statsmodels · WandB · SQL · transfer learning · representation learning · variational autoencoders · attention pooling · custom loss functions · mixed precision (bfloat16) · gradient checkpointing · genomic foundation models (Enformer, Borzoi, Evo2)

Statistics & genomics: regression modelling · nested cross-validation · partial correlation · hypothesis testing · bootstrap CIs · multiple-testing correction · Bayesian inference (MCMC) · GWAS/PWAS · SNP heritability (GCTA-GREML) · in silico mutagenesis · variant calling (GATK) · variant annotation · sequence alignment · PLINK · pysam · bcftools

Computing & infrastructure: SLURM (HPC clusters) · Linux/bash · Git/GitHub · HDF5/h5py · Docker · Nextflow · AWS (Batch, S3, ECR, IAM)

Wet lab: LC-MS/MS · Western blotting · organic synthesis · mutagenesis · protein expression and purification