KELLY A. MCGLYNN, PH.D.

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HIGHLIGHTS

- Pharmacology Ph.D. with a background in cancer epigenetics (leukemia) and hematology. 2 years industry experience post-Ph.D. and 7 years total research experience in oncology. Broad technical skill set to adapt to project needs.
- Industry experience performing FACS sorting on human PBMC samples and optimizing experimental protocols for single-cell RNA sequencing. Expert in standard molecular biology techniques, with 7 years tissue culture experience, including adherent, suspension and primary cells; transfection, lentiviral infection, and cell culture assays using primary bone marrow progenitor cells.
- Experience with *in vivo* models (mouse models of leukemia and normal hematopoiesis), animal techniques including genotyping and tissue harvesting, and design of long-term *in vivo* experiments with multiple time points.
- *Writing & Communication*: Published an abstract accepted for ASCO 2021. Presented research progress regularly at 1:1 and translational group meetings. Independently wrote a successful NIH fellowship grant during Ph.D. Supervised and trained 14 undergraduate and junior graduate students in basic research methods and molecular techniques.

TECHNICAL SKILLS

Disease area expertise	Hematology, Oncology (leukemia), normal hematopoiesis, epigenetics.
Cell Biology	Flow cytometry (up to 8 colors) and fluorescent cell sorting (BD Fortessa and Sony SH800 sorter), sample prep/staining, lineage depletion using magnetic beads.
	7 years experience with mammalian cell culture (adherent, suspension and primary bone marrow progenitor cells). Transfection, shRNA, lentiviral and retroviral production and infection, cell culture functional assays (differentiation, hematopoietic colony formation).
Oncology & *in vivo* biology	Mouse models of leukemia, mouse handling, isolation of primary bone marrow and other tissues, bone marrow transplantation, genotyping and colony management, cytospins.
Molecular Biology & Biochemistry	7 years molecular biology and cloning experience; DNA/RNA purification, PCR, qPCR/RT-PCR. SDS-PAGE, Western blot, immunoprecipitation. **Epigenetics-specific techniques: ChIP-qPCR, histone methyltransferase assays*
Software	Robotic liquid handling platforms: Tecan, Agilent Bravo and Formulatrix MANTIS
	Graphpad Prism, FlowJo, FACS Diva, DNA/cloning software (Snapgene, SeqBuilder).
Data Science & Coding	Python coding, data cleaning and processing (pandas, numpy), conda, Jupyter notebooks.

EDUCATION

2018 **Ph.D.**, Pharmacology, *University of Rochester Medical Center, Rochester, NY*
- *Grants & Honors:* Awarded NIH NCI F31 Individual Predoctoral Fellow, NIH T32 Grant Trainee

2012 **B.S.**, Molecular Biology, *University of Wisconsin – La Crosse, La Crosse, WI*

EXPERIENCE

Feb 2022 - Present | **Scientist II, Discovery Biology**
MOMA Therapeutics, Cambridge, MA

- Discovery biologist on 2 pre-clinical oncology small molecule discovery programs.
- Designing and performing experiments focused on target engagement, biomarker development, and mechanism of action.
- Managing external studies at CRO partners.

May 2021 – Feb 2022 | **Scientist I, Translational Biology**
Constellation Pharmaceuticals, Cambridge, MA

- Scientist in the Translational Research department, focused on mechanism of action and biomarker research related to ongoing Phase 3 trial (small molecule BET inhibitor) for the treatment of myeloproliferative neoplasms.
- Set up and optimized a TARGETseq protocol (single-cell RNA and genomic sequencing) for the analysis of clinical trial patient PBMC samples, pre- and post-treatment. Designed and tested a 6-color sorting panel and sorted primary human hematopoietic progenitor cells into 384-well plates. Optimized PCR and targeted cDNA amplification and designed primer multiplexing strategies according to patient mutational status. Utilized Agilent Bravo and MANTIS robotic liquid handling platforms to automate 384-well plate processing, including adding lysis buffer, primer mixes, and PCR master mixes.
- Performed *ad hoc* bioinformatics analyses of pre-processed RNAseq data to investigate genes of interest for potential validation studies.
- Attended virtual conferences on hematological malignancies, internal journal clubs, and presented research progress at small group meetings on an ongoing basis.

Jun 2020 – Apr 2021 | **Clinical Oncology Analyst**
IntrinsiQ Specialty Solutions (AmerisourceBergen), Boston, MA

- Clinical data analyst focused on providing custom analytics to pharma clients on oncology drug utilization, sales, and clinical trends for oral and IV chemotherapies.
- Participated in a cross-functional team project to develop a new software platform for clinical trials site selection. Wrote an automated reporting pipeline in Python to validate projected patient drug usage data.
- Attended virtual conferences on precision medicine, biomarker testing and emergent cancer therapies. Submitted an ASCO abstract on biosimilar utilization based on analysis of real-world drug administration data and trends in provider prescribing.

Jan 2020 – Apr 2020 | **Insight Health Data Science Fellow** *(3-month fellowship program)*
Insight Data Science, Boston, MA

2019 – 2020 | **Postdoctoral Researcher**
Department of Genetics (Paula Vertino Lab), Wilmot Cancer Center, Rochester, NY

- Research on epigenetic and TGF-beta-driven mechanisms in breast cancer oncogenesis. Performed drug treatments, flow cytometry and Western blot analysis on breast cancer cell lines. Designed and created stable CRISPR knockout cell lines and screened clones via Western blot, sequencing and T7 mismatch repair assay.
- Performed pilot experiments to test whether a small molecule compound could reduce surface PD-L1 (via flow cytometry) in lung and breast cancer cell lines.
- Designed and performed a single-cell RNA sequencing experiment to investigate differences in gene expression during the cellular transition from a normal to invasive state.

2012 – 2018 | **Ph.D. Student**
Department of Pathology (Archibald Perkins Lab), University of Rochester Medical Center, Rochester, NY

- Translational research on the role of MDS1-EVI1/Prdm3 in hematopoiesis and leukemogenesis.
- Independently wrote a successful 3-year NIH National Cancer Institute (NCI F31) fellowship grant, including literature review, experimental approach, potential pitfalls and alternative approaches.
- Designed, cloned and contributed 7 custom recombinant DNA plasmids to the global plasmid repository Addgene, which have been requested 60+ times and shipped to labs around the world.

Graduate Research Projects:

EVI1 interacts with the SWI/SNF subunit BAF57 in acute leukemia.

- Developed a novel epitope-tagged leukemic mouse model overexpressing PRDM3/EVI1. Performed serial bone marrow transplantation into irradiated recipient mice to expand leukemic cells. Harvested spleen tissue from transplant recipient mice to perform epitope tag pulldowns and mass spectrometry analysis.
- Identified a novel protein-protein interaction between EVI1 and the SWI/SNF chromatin remodeling complex in leukemic tissue and confirmed the interaction via co-IP in multiple cell types.
- Employed ChIP-qPCR to confirm novel co-localization between EVI1 and the SWI/SNF chromatin remodeling complex.

***Prdm3* and *Prdm16* cooperatively maintain hematopoiesis with dependence on the PR domain**

- Initiated project to generate and characterize a novel tamoxifen-inducible double knockout mouse with a bone marrow failure phenotype; performed flow cytometry analysis of bone marrow, blood smears and cell culture assays on primary bone marrow precursor cells.
- Performed *in silico* structural analysis of the putative enzymatic domain, examining evolutionary conservation in the binding pockets, predicted potential catalytic residues as targets for point mutations.
- Established a cell culture functional assay (soft agar colony formation assay) to demonstrate that addback of wild-type *Prdm3* or *Prdm16*, but not *Prdm3* with specific point mutations in its putative enzymatic domain, rescues the phenotype.

PUBLICATIONS AND PRESENTATIONS

Zhang Y, McGrath KE, Ayoub E, Kingsley PD, Yu H, Fegan K, McGlynn K., Rudzinskas S, Palis J, Perkins AS. **(2021).** Mds1^{CreERT2}, an inducible Cre allele specific to adult-repopulating hematopoietic stem cells. *Cell Rep.2021 Aug 17;36(7):109562. doi: 10.1016/j.celrep.2021.109562.*

McGlynn K., Pack L., Ayoub E., Chatterjee G., Zhang Y., and Perkins AS. Development of a mouse model to investigate EVI1-containing protein complexes in leukemic tissue: characterization of interaction with SWI/SNF complex. *[Publication submitted March 2021]*

McGlynn K., McGarry J., Clinton N., and Patel KB. (**2021**). Trends in biosimilar prescribing and pricing among oncology providers, 2019-2020. *[Abstract, accepted to ASCO 2021].*

McGlynn K., Sun R., Vonica A., Rudzinskas S., Zhang Y., and Perkins AS. (**2020**). *Prdm3* and *Prdm16* cooperatively maintain hematopoiesis with dependence on the PR domain. *Experimental Hematology, 85, 20–32.e3. https://doi.org/10.1016/j.exphem.2020.04.010.*

Malek, A., McGlynn, K., Taffner, S., Fine, L., Tesini, B., Wang, J., Mostafa, H., Petry, S., Perkins, A., Graman, P., *et al*. (**2019**). Next-Generation-Sequencing-Based Hospital Outbreak Investigation Yields Insight into Klebsiella aerogenes Population Structure and Determinants of Carbapenem Resistance and Pathogenicity. *Antimicrobial agents and chemotherapy 63*.

Ph.D. Thesis, available online: McGlynn K. *Cooperative and mechanistic roles of Mecom in hematopoiesis.* University of Rochester; **2018**. http://hdl.handle.net/1802/34859.

McGlynn K., Sun R., Vonica A., Rudzinskas S., Zhang Y., and Perkins AS. Prdm3 and Prdm16 contribute to hematopoietic stem cell regulation. (*Poster, national Keystone Symposium on Epigenetics & Cancer*) (**2017**) .

McGlynn K., Zhang, Y., and Perkins, A. Characterization of Prdm3-containing protein complex in MLL leukemia. (*Poster, national EpiCypher conference on Clinical Frontiers in Epigenetics*) (**2016**).

McGlynn K., Zhang, Y., and Perkins, A. The Zinc Finger Transcription Factor Mds1-Evi1 Forms a Novel Protein Complex in MLL leukemia. (*Poster, national Keystone Symposium on Epigenetics & Cancer*) (**2015**).