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KELLY A. MCGLYNN, PH.D.

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HIGHLIGHTS

- Motivated and determined scientist with 1 year post-PhD experience and **6 years total research experience in cancer epigenetics** (hematology). Broad technical skill set to adapt to project needs.
- Experienced with ***in vivo* oncology models** (mouse models of leukemia and normal hematopoiesis) and animal techniques, including harvesting of various tissues and **multicolor flow cytometry**. Performed **primary-cell assays** on murine bone marrow precursor cells.
- 6 years molecular cloning experience: designed and cloned 20+ mammalian and bacterial expression vectors customized with epitope tags, fluorescent or selectable markers. Designed a **CRISPR** experiment for a breast cancer cell line, generating a novel knockout cell line.
- Independently wrote a successful NIH pre-doctoral fellowship grant and submitted progress reports.
- Individually supervised, trained and provided mentorship to 11 undergraduate and junior graduate students. Able to collaborate and communicate across disciplines and looking forward to working on a team. Will thrive in a fast-paced environment!
- *Looking to permanently relocate!*

EDUCATION & EXPERIENCE

Postdoctoral Researcher (December 2018 – Present)
Wilmot Cancer Center, University of Rochester

- *Drug Discovery* by University of California San Diego on Coursera (June 2019).
- *Data Science Specialization,* set of 10 courses on data analysis and programming in R (Johns Hopkins), *in progress*

Ph.D. in Pharmacology (October 2018)
University of Rochester Medical Center, Rochester, NY

- *Grants:* NIH F31 Predoctoral Fellowship, Trainee on NIH T32 Training Grant, Dean's Travel Award

B.S. in Molecular Biology, Minor in Chemistry (2012)
University of Wisconsin-La Crosse, La Crosse, WI

POSTDOCTORAL RESEARCH

Using a small molecule inhibitor of the H4K20 methyltransferase Suv420h2 to identify Suv420h2-regulated genes in breast cancer. Project goals:

- Designed a CRISPR experiment to generate a knockout MCF7 breast cancer cell line. Tested transfection of single vs. multiple combined sgRNAs. Screened and confirmed knockout clones via genomic DNA sequencing, Western blot and T7 mismatch cleavage assay.
- Analyzed whether a small molecule compound could reduce surface PD-L1 (flow cytometry) in lung and breast cancer cell lines.

GRADUATE RESEARCH

Discovered a novel protein-protein interaction between a transcription factor and a chromatin remodeling complex

- Developed an acute leukemia mouse model to identify protein-protein interactions in leukemic tissue. Performed pulldowns and mass spec, identifying a novel protein-protein interaction between the transcription factor EVI1 and multiple subunits of the chromatin remodeling complex SWI/SNF.
- Confirmed the interaction via co-IP in primary cells and cell lines, and employed ChIP-qPCR to confirm genomic co-localization at the transcription factor's DNA binding sites.

Characterized a double knockout mouse model with a bone marrow failure phenotype

- Initiated project to generate a tamoxifen-inducible double knockout of the homologous transcription factors *Prdm3* and *Prdm16*. Assisted with tamoxifen injections. Harvested bone marrow from long bones, prepared bone marrow touch prep and cytospin slides, and analyzed myeloid precursor and mature bone marrow subsets via 7+-color flow cytometry.
- Established a cell culture functional assay (soft agar colony formation assay) in primary bone marrow cells to demonstrate that retroviral addback of the wild-type *Prdm3* gene, but not *Prdm3* with specific point mutations in its putative enzymatic domain, rescues the phenotype. Performed *in silico* structural analysis of the putative enzymatic domain to predict the potential consequences of point mutations on the ligand binding site.

Analysis of mutations in bacterial porins in clinical outbreak strains of carbapenem-resistant Enterobacter aerogenes [Collaboration project]

- Collaborated with a clinical microbiologist on a study of mutations in antibiotic-resistant bacteria from hospital patient isolates. Performed *in silico* structural analysis (PyMOL) and alignments of antibiotic importer proteins to predict the potential functional significance of point mutations for bacterial antibiotic resistance.

TECHNICAL SKILLS

- Molecular Biology: Designed and engineered 20+ plasmid constructs during Ph.D.; mutagenesis, PCR, qPCR, CRISPR/Cas9 gene editing and screening. Contributed 7 plasmids to Addgene (June 2018), which have been requested 34 times.
- Biochemistry: Bacterial protein expression and purification, SDS-PAGE, Western blot, fluorescent DNA-binding assays, anisotropy/fluorescence polarization, ELISA-based enzyme activity assay, immunoprecipitation and protein-protein interaction studies.
- Cell biology: Cell culture functional assays (cell cycle, differentiation, hematopoietic colony formation), multicolor flow cytometry; culture of primary cells, adherent, and suspension cell lines; transfection; shRNA, lentiviral and retroviral infections.
- Cancer & *in vivo* biology: Isolation of bone marrow and splenocytes from mice, blood & bone marrow smears, mouse models of leukemia, CBC, isolation of primary murine thymocytes, spheroid culture.
- Epigenetics: ChIP-qPCR, histone methyltransferase assays, nucleosome reconstitution, *in vitro* SWI/SNF nucleosome remodeling assays.
- Software: Intermediate-level R and Python programming. Graphpad Prism, FlowJo, PyMOL, DNA/cloning software (Snapgene, SeqBuilder), mouse colony database software.

PUBLICATIONS AND PRESENTATIONS

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* cooperatively maintain hematopoiesis with dependence on the PR domain. *[Submitted to Haematologica – impact factor 7.7]*

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)