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KELLY A. MCGLYNN, PH.D.

EXECUTIVE SUMMARY AND ACCOMPLISHMENTS

- Creative scientist with a background in cancer biology, highly motivated to apply my skills to contribute to a industry drug discovery and development team. Broad technical skill set to adapt to project needs. Seeking a career in early development and discovery of new therapeutics.
- Strong experience in cell biology and biochemistry techniques, including cell culture assays, flow cytometry, and fluorescence microscopy.
- 5 years experience in independent experimental design and development of protocols to address research questions.
- Able to collaborate and communicate across disciplines, and looking forward to working in a team. Will thrive in a fast-paced environment!

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).

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
- *Key coursework:* Leadership & Management for Scientists (2017), Critical Thinking (2016)

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:
- Use CRISPR/Cas9 editing to insert a genomic Suv420h2 epitope tag in MCF7 breast cancer cells to determine specific target genes of Suv420h2.
- Determine whether small molecule inhibition of Suv420h2 can sensitize breast cancer cells to chemotherapeutic agents or modify drug resistance.

GRADUATE RESEARCH

EVI1 interacts with the SWI/SNF subunit BAF57 in acute leukemia.
- Developed a novel epitope-tagged leukemic mouse model overexpressing PRDM3/EVI1, used this model to identify protein interactions via pulldown 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 mouse model containing tamoxifen-inducible double knockout of two transcription factor genes involved in hematopoiesis, *Prdm3* and *Prdm16*.
- Coordinated data collection in collaboration with other team members to characterize the bone marrow failure phenotype of double knockout mice.
- 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.

- Performed *in silico* structural analysis of the putative enzymatic domain, examining evolutionary conservation in the binding pockets, predicted catalytic residues, and potential consequences of our specific addback point mutations on PRDM3's ligand binding sites.

[Collaboration project] **Analysis of AmpD enzyme and Omp36 porin mutations in clinical outbreak strains of carbapenem-resistant *Enterobacter aerogenes***

- Performed *in silico* structural analysis (PyMOL) of antibiotic importer proteins with clinical strain mutations to predict the potential functional significance of point mutations for bacterial antibiotic resistance.

TECHNICAL SKILLS

- Molecular Biology: Molecular cloning: designed and engineered 15+ plasmid constructs during Ph.D.; mutagenesis, PCR, qPCR.
- Biochemistry: Protein purification (from bacteria, mammalian cells and mouse tissue), SDS-PAGE, Western blot, fluorescent DNA-binding gel shift assays, anisotropy/fluorescence polarization small molecule binding assays, ELISA-based enzyme activity assay, immunoprecipitation and protein-protein interaction studies.
- Cell biology: Cell culture functional assays (MTT assay, 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, cell line spheroid culture.
- Epigenetics: ChIP-qPCR, histone methyltransferase assays, nucleosome reconstitution, *in vitro* SWI/SNF nucleosome remodeling assays.
- Software: Graphpad Prism, FlowJo, PyMOL, DNA/cloning software (Snapgene, SeqBuilder), mouse colony management software.

PUBLICATIONS AND PRESENTATIONS

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*) (2017)

Keystone Symposium: Epigenetics and Human Disease: Progress from Mechanisms to Therapeutics, Seattle, WA, January 2017.

McGlynn K., Zhang, Y., and Perkins, A. Characterization of Prdm3-containing protein complex in MLL leukemia. (*Poster*) (2016)

EpiCypher 2016: Biological and Clinical Frontiers in Epigenetics, San Juan, Puerto Rico, April 2016.

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

Keystone Symposium on Epigenetics and Cancer, Keystone, CO, January 2015.

Poster abstract published online: The FASEB Journal *29* (2015).

Acknowledged for contributions to: Papasergi-Scott, M. M., *et al*. (2018). *Science Signaling* 11(532).