# JAMES RENNIE BEQUEST

## REPORT ON EXPEDITION / PROJECT / CONFERENCE

**Expedition/Project/ Conference Title:** EMBL Conference: Transcription and chromatin (6319)

**Travel Dates:** 26 – 31 August 2022

**Location:** Heidelberg, Germany

**Group member(s):** Ning Zhao

**Aims:** Give a poster presentation of my PhD work.
Network with other researchers in the chromatin modification field.

---

EMBL Conference on transcription and chromatin held in Germany in August 2022. This biennial meeting is one of the most prestigious conferences in our field and has played a long-standing role in shaping the field of the transcriptional regulation. The meeting brings together leading experts covering all aspects of transcription including cis-regulatory function, long-range regulation, 3-dimensional looping, the basal transcriptional machinery, RNA polymerase regulation and function, nucleosome positioning, chromatin modifications, chromatin remodelling and epigenetic inheritance of transcriptional silencing. The programme consists of talks selected from submitted abstracts that are interspersed with invited speakers, discussing the latest breakthroughs in transcriptional regulation. Attending this EMBL meeting gave me an invaluable opportunity to present my work to the international community and receive feedback as I prepare to write a manuscript for publication. I also got the chance to hear and learn first-hand about the latest developments in the field, and to make valuable contacts outside of the Edinburgh that will help me prepare for the next step in my research career.

I am specifically interested in chromatin modification and epigenetic inheritance of transcriptional silencing, as my PhD project involves investigation of the role SUMO (small ubiquitin-related modifier) plays in heterochromatin formation in fission yeast. Based on my previous data, I managed to deduce that SUMO plays a role via the chromodomain of the sole fission yeast H3K9 methyltransferase Clr4. However, it is still unknown whether this is mediated by an alteration to the structure of Clr4, or whether Clr4's interactions with other heterochromatin proteins are disrupted. I was hoping to use the conference as an opportunity to speak to some structural biologists to get their perspectives on how SUMO may be impacting the function of Clr4.There were a number of talks that really fascinated me, which described the mechanism that underlies gene transcription and its regulation in chromatin. The speakers have uncovered the structure of the human transcription preinitiation complexes containing RNA polymerase II and the mediator, of Pol II elongation complexes in paused pre-

termination and active states, and of Pol II complexes with parts of the spliceosome and the DNA repair machinery.

Studies have indicated that SUMO modification is a transient and dynamic process, which makes studying this modification challenging. I have always been keen to understand which step of heterochromatin formation SUMO modification plays a role in, therefore a dynamic system will help to dissect the role that SUMO plays in this process. The other talk that interested me most was about the modulation of gene expression dynamics by transiently active regulatory elements. In this talk, they studied gene repression in a system that allows dynamic control of the erythroid transcription factor GATA1. One of the key GATA1 targets for silencing is the proliferative gene Kit, which has been repressed for erythroid precursors to exit the cell cycle and terminally differentiate. They presented that H3K27ac, production of noncoding transcripts likely representing enhancer RNAs (eRNAs), and long-range interactions with the Kit promoter-proximal region. Strikingly, these elements only exist transiently as they are eventually erased upon complete Kit silencing. The speakers also used PRO-seq experiments to measure eRNAs, along with H3K27ac profiling, indicating that similar transient enhancer-like elements exist at numerous genes undergoing silencing.

During the poster sessions, dinners and free time, I was able to network with experts in the field of the chromatin modification and exchange my views with different people coming from different perspectives. Overall, I enjoyed this conference very much. I am really grateful to the James Rennie Bequest for supporting my attendance at this conference.