



## Illinois Wesleyan University Digital Commons @ IWU

---

John Wesley Powell Student Research  
Conference

2007, 18th Annual JWP Conference

---

Apr 14th, 9:00 AM - 10:00 AM

# Histone Modification Patterns Across the X Centromere Reflect Genomic Environment

Kristen Kopf, '08

*Illinois Wesleyan University*

Beth A. Sullivan, Faculty Advisor

*Illinois Wesleyan University*

Follow this and additional works at: <http://digitalcommons.iwu.edu/jwprc>

---

Kristen Kopf, '08 and Beth A. Sullivan, Faculty Advisor, "Histone Modification Patterns Across the X Centromere Reflect Genomic Environment" (April 14, 2007). *John Wesley Powell Student Research Conference*. Paper 31.  
<http://digitalcommons.iwu.edu/jwprc/2007/posters/31>

This Event is brought to you for free and open access by The Ames Library, the Andrew W. Mellon Center for Curricular and Faculty Development, the Office of the Provost and the Office of the President. It has been accepted for inclusion in Digital Commons @ IWU by the faculty at Illinois Wesleyan University. For more information, please contact [digitalcommons@iwu.edu](mailto:digitalcommons@iwu.edu).

©Copyright is owned by the author of this document.

Poster Presentation P49

**HISTONE MODIFICATION PATTERNS ACROSS THE X CENTROMERE  
REFLECT GENOMIC ENVIRONMENT**

Kristen Kopf and Beth A. Sullivan\*  
Biology Department, Illinois Wesleyan University  
and Duke University

Centromeres, the primary point of constriction on chromosomes, are essential for proper chromosome segregation during meiosis and mitosis. Due to their large sizes and repetitive DNA content, centromere regions have been excluded from genome projects. However, being such fundamental functional elements that are epigenetically regulated, we want to understand their genomic organization and the relationship between underlying DNA sequence and chromatin and protein organization. In collaboration with a colleague at NHGRI, we are using chromatin immunoprecipitation-PCR (ChIP-PCR) to generate epigenomic profiles that overlay histone modifications onto the centromeric-pericentromeric genomic assemblies from human-mouse hybrid chromosomes. Our findings indicate that centromeric chromatin organization is regulated via epigenetic factors rather than wholly DNA sequence. This information is being used to identify genomic features that structurally, and potentially functionally, separate the centromere from the rest of the genome.