

Development of a standards-driven genomic mapping platform to measure acute Pol II response dynamics



James T. Anderson¹, Allie R. Hickman¹, Alexandra C. Nowlan², Morgan Oatley¹, Marcus A. Cheek¹, Matthew J. Meiners¹, Zoe A. McElligott², Michael-Christopher Keogh¹ & Bryan J. Venters¹

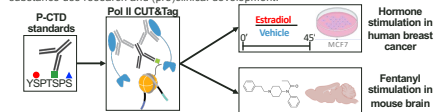
¹ EpiCypher Inc., Research Triangle Park, Durham NC 27709, USA
² Department of Psychiatry, University of North Carolina, Chapel Hill, NC, USA.

Abstract & Graphical Overview

Acute transcriptional responses are essential for normal development and homeostasis. However, current approaches to study transcription dynamics have significant limitations. To overcome these limitations, we have developed a CUT&Tag-based approach to directly and quantitatively profile chromatin-engaged RNA polymerase II (Pol II).

For assay development, we screened nearly 40 commercial Pol II antibodies for specificity / efficiency via our phospho-CTD- α standards. Strikingly, for many antibodies, epitope recognition was weakened or completely masked when adjacent phospho-marks were present. In addition, most antibodies tested displayed a strong preference for the corresponding double modification versus its singly-modified counterpart.

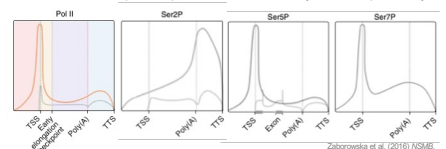
The best performing reagents were used to benchmark Pol II CUT&Tag in MCF7 breast cancer cells stimulated by estradiol. Finally, optimized Pol II CUT&Tag was used to investigate transcriptional dynamics within an hour after opioid exposure. Cohorts of mice were treated with a fentanyl time-course; and brain tissue harvested, fixed and dissociated to isolate nuclei from striatal neurons. Subsequent Pol II CUT&Tag identified opioid-regulated genes and tracked their transcriptional dynamics over time of opioid exposure. Overall, Pol II CUT&Tag is a sensitive and scalable approach that will revolutionize the study of transcriptional dynamics in complex tissues, supporting substance use research and (pre)clinical development.



Distinguishing Pol II phospho-CTD dynamics critically depends upon antibody performance

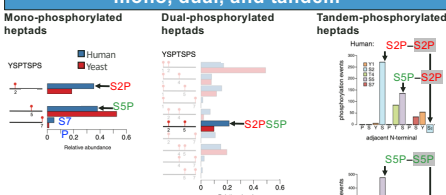
Canonical CTD heptad: YSPTSPS

- 52x and 26x heptad repeats in human and yeast, respectively



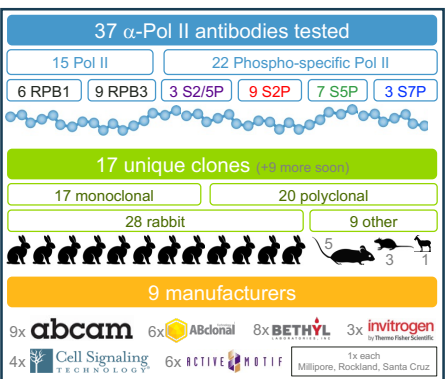
However, the specificity, efficiency, and masking effects of antibodies for Pol II CTD phospho-forms are not fully understood.

Phospho-CTD marks exist in all three forms: mono, dual, and tandem

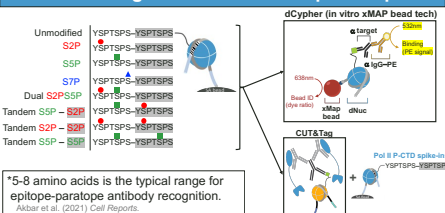


Functional unit of RNA Pol II CTD lies within heptad-pairs

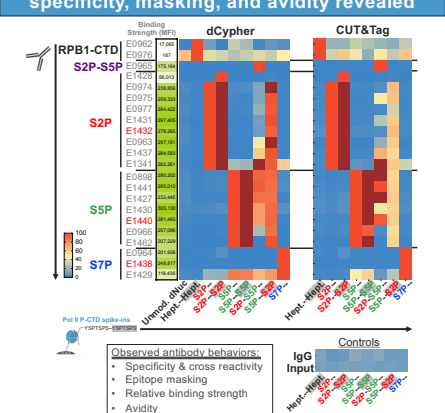
YSPTSPS-YSPTSPS
 Siller & Cook (2004) Euk. Cell.
 Shah et al. (2019) Biol. Lett.
 Appel et al. (2021) Nat. Commun.



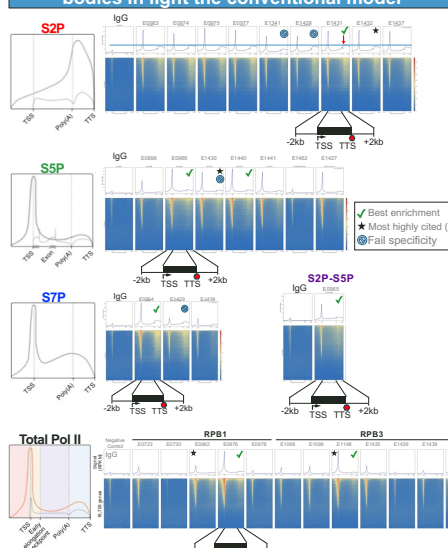
Rational design of Pol II P-CTD spike-in panel



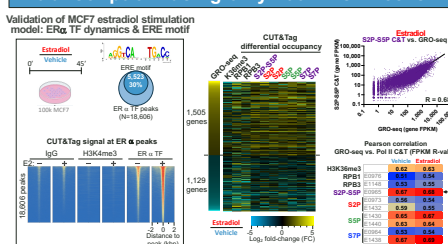
Insights from Pol II antibody characterization: specificity, masking, and avidity revealed



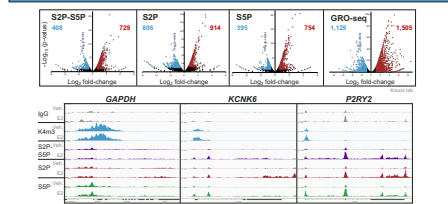
Pol II P-CTD enrichment patterns across gene bodies in light the conventional model



Pol II P-CTD CUT&Tag is a proxy for nascent transcription: using only 100k MCF7 cells

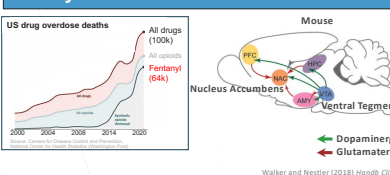


P-CTD dynamics in MCF7 estradiol model

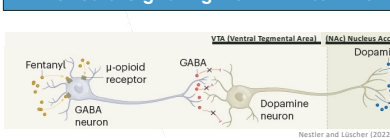


Acute Pol II dynamics in fentanyl-stimulated neurons

Dopamine reward circuit is central to the fentanyl overdose death crisis

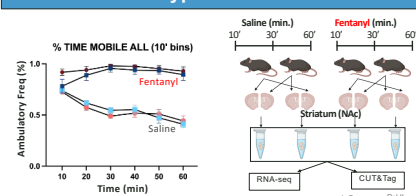


Fentanyl hijacks the dopamine reward circuit: signaling from VTA to NAc

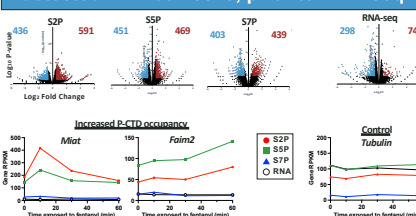


How does fentanyl impact transcriptional and epigenetic pathways in the NAc?

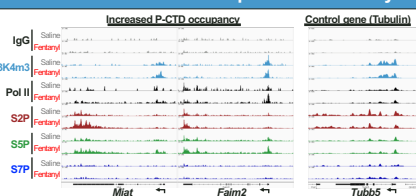
Mice injected with fentanyl become acutely hyperactive



Fentanyl stimulation: acute P-CTD dynamics detected in <100k cells, prior to RNA-seq



Genome browser view of genes with increased P-CTD in response to fentanyl



Pol II phosphorylation dynamics linked to morphine addiction circuit & neural plasticity

