





Medical Microbiology and Immunology MMI 291 Seminar Series

Emerging Challenges in Microbiology and Immunology Current Theme: Interdisciplinary Research



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"Transcriptional control by readers

and writers of the Histone Code"

Friday, November 30, 2018 Genome and Biomedical Sciences Facility, Auditorium Room 1005 12:10 PM – 1:00 PM

Research work: Dr. Strahl's lab is interested in the role that histone post-translational modifications have in chromatin biology. Specifically, they are studying how enzymes that 'write' and 'read' histone modifications contribute to the function of chromatin and DNA-templated functions like gene transcription. To do so, they are employing a range of model organisms (yeast to mammalian cells) and approaches (genomics, genetics, biochemistry, biophysics as well as proteomics) that, together, are elucidating how readers and writer enzymes function to sculpt the chromatin landscape and regulate gene transcription.

Publication references:

Dronamraju, R., Hepperla, A. J., Shibata, Y., Adams, A. T., Magnuson, T., Davis, I. J. & Strahl, B. D. (2018) Spt6 association with RNA Polymerase II directs mRNA turnover during transcription. Mol Cell. 70:1054-1066

Dronamraju, R., Jha, D., Eser, E., Dominguez, D., Adams, A., Choudhury, R., Chiang, Y. C., Rathmell, W. K., Emanuele, M. J., Churchman, L. S. & Strahl, B. D. (2018) Set2 methyltransferase facilitates cell cycle progression by maintaining transcriptional fidelity. Nucleic Acids Res 46:1331-1344.

Shanle, E. K.*, Shinsky, A. A.*, Bridgers, J. B., Bae, N., Sagum, C., Krajewski, K., Rothbart, S. B., Bedford, M. T.* & Strahl, B. D.* (2017) Histone peptide microarray screen of chromo and Tudor domains defines new histone lysine methylation interactions. Epigenetics & Chromatin 10:12. doi: 10.1186/s13072-017-0117-5.