**Haitao Li**

**Ph.D, Professor**



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**Employment and Education：**

2010.1-present Professor, School of Medicine, Tsinghua University

2003.10-2010.1 Research Fellow, Research Associate (2005.8), and Senior Research Scientist (2006.11), Structural Biology Program, Memorial Sloan-Kettering Cancer Center, New York, USA

1997.9-2003.7 Ph.D. in Molecular Biophysics, Institute of Biophysics, CAS

1993.9-1997.7 B.Sc. in Microbiology, Department of Microbiology, Shandong University

**Research Summary:**

Dr. Li’s research is directed towards a molecular understanding of epigenetic regulations - the way our genetic information is organized and decoded at chromosomal level. Epigenetic mechanisms involve chemical modifications to histones or DNA, histone variants, chromatin remodeling, and non-coding RNAs. Growing evidence shows that epigenetic regulations play key roles in many biological processes, and it has become clear that their dysregulation can give rise to diverse diseases, notably cancer. The Li laboratory mainly applies macromolecular X-ray crystallography amongst other modern biophysical or biochemical techniques to study the structure and function of key epigenetic regulators, with an ultimate goal for epigenetic drug discovery. His major achievements in the past have been to elucidate the molecular basis for histone modification readout by a wealth of "reader" modules or their combinations. Examples include PHD finger (*Nature*, 2006), WD40 repeats (*Nat Struc & Mol Biol*, 2006), MBT (*Mol Cell*, 2007), PHD-Bromo (*Cell*, 2010, 2011), ADD (*Nat Struc & Mol Biol*, 2011), Spin/Ssty repeats (*Genes Dev*, 2014), Bromo-PWWP (*Nature*, 2014) and YEATS domain (*Cell*, 2014).

**Selected Publications （out of 34）:**

1. Li Y, Wen H, Xi Y, Tanaka K, Wang H, Peng D, Ren Y, Jin Q, Dent SYR, Li W, **Li H\***, and Shi X\* (2014) AF9 YEATS domain links histone acetylation to DOT1L-mediated H3K79 methylation. ***Cell*** 159(3):558-571 (\*correspondence)
2. Wen H, Li, Y, Xi Y, Jiang S, Stratton S, Peng D, Tanaka K, Ren Y, Xia Z, Wu J, Li B, Barton MC, Li W\*, **Li H**\*, and Shi X\* (2014) ZMYND11 links histone H3.3K36me3 to transcription elongation and tumor suppression. ***Nature*** 508(7495):263-268. (\*correspondence)
3. Su X, Zhu G, Ding X, Lee SY, Dou Y, Zhu B, Wu W\*, and **Li H\*** (2014) Molecular basis underlying histone H3 lysine-arginine methylation patter readout by Spin/Ssty repeats of Spindlin1. ***Genes Dev*** 28:622-636. (\*correspondence)
4. Zheng X, Gooi, LM, Wason A, Gabriel E, Mehrjardi NZ, Yang Q, Zhang X, Debec A, Basiri M, Avidor-Reiss T, Pozniakovsky A, Poser I, Saric T, Hyman AA, **Li H**\* and Gopalakrishnan J\* (2014) The conserved TCP domain of Sas-4/CPAP is essential for Peri-centriolar material tethering during centrosome biogenesis. ***Proc Natl Acad Sci USA*** 111(3): E345-E363 (\*correspondence)