Toyotaka Ishibashi

Division of Life Science,

The Hong Kong University of Science and Technology, HK

Email: toyotaka@ust.hk

Selected Publication

Ishibashi T.[*#], Dangkulwanich M.[*], Coello Y.[*], Lionberger T.A., Lubkowska L., Ponticelli A.S., Kashlev M., Bustamante C[#]. (2014) Complete dissection of transcription elongation reveals slow translocation of Pol II in a linear ratchet mechanism, *Proc. Natl. Acad. Sci. USA*, 111(9), 3419-24.

[*]co-first author, [#]corresponding author

Research Aims and Interests

Our lab is interested in transcription regulation mechanisms in a dynamic cell nucleus environment. While transcription by RNA polymerase can occur on bare DNA *in vitro*, the RNA polymerase encounters much more complicated environment *in vivo*.

We would like to elucidate the mechanisms how transcription regulation is affected by processes including chromatin remodeling, DNA damage and DNA repair.

The biological functions of histone variants

Histones variants are non-canonical variants of histones that have specific expression patterns and functions such as transcription initiation by H2A.Z and DNA repair response by H2A.X. In our lab, we are particularly interested in characterizing the roles of testes-specific histone variants (e.g. H2A.Bbd, TH2B, H3t etc.) using a combination of biochemical, biophysical and cell biological methods.

Molecular dynamics of chromatin remodelers

Chromatin remodeler modulates chromatin structure by relocating nucleosomes' position using energy of ATP hydrolysis. We are using single-molecular approaches to study the dynamics of chromatin remodeling enzymes and their roles in transcription.