

# Publications

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## Recent Publications

1. Sandhu *et al.*,  
“Large-scale Functional Organization of Long-Range Chromatin Interaction Networks”,  
**Cell Rep.**, 2012. PDF.
2. The ENCODE Project Consortium, “An Integrated Encyclopedia of DNA Elements in the Human Genome”,  
**Nature**. 2012. ENCODE Website.
3. Djebali *et al.*,  
“Landscape of Transcription in Human Cells”,  
**Nature**. 2012. ENCODE Website.
4. Li, G., *et al.*,  
“Extensive Promoter-centered Interactions provide Higher-order Framework for Transcription Regulation in Human Cells”,  
**Cell**. 2012. PDF.
5. Goh, Y., **Fullwood, M.J.**, Poh, H.M., Peh, S.Q., Ong, C.T., Zhang, J.Y., , Ruan, X., Ruan, Y.,  
“Chromatin Interaction Analysis with Paired-End Tag Sequencing (ChIA-PET) for mapping chromatin interactions and understanding transcription regulation”,  
**J. Vis. Exp.** 2012. Link.
6. **Fullwood, M.J.**, Lee, J., Lin, L., Li, G., Huss, M., Ng, P., Sung, W-K., and Shenolikar, S.,  
“Next-generation Sequencing of Apoptotic DNA Breakpoints Reveals Association with Actively Transcribed Genes and Gene Translocations”,  
**PLoS ONE**. 2011. PDF.
7. **Fullwood, M.J.**, Han, Y.Y., Wei, C.L., Ruan, X., Ruan, Y.  
“Chromatin Interaction Analysis using Paired-End Tag Sequencing”,  
**Current Protocols in Molecular Biology**. 2010. PDF.
8. Li, G., **Fullwood, M.J.**, Han X., *et al.*  
“ChIA-PET Tool for Comprehensive Chromatin Interaction Analysis with Paired-End Tag

Sequencing”,  
**Genome Biology**. 2010. PDF.

9. **Fullwood, M.J., et al.**  
The Oestrogen Receptor  $\alpha$ -mediated Human Chromatin Interactome,  
**Nature**. 2009. PDF. Supplement.
10. **Fullwood, M.J.,** Wei, C.L., Liu, E. T. and Ruan, Y.  
Ultra-High-Throughput Sequencing of Paired-End Tags (PET) for Transcriptome and  
Genome Analyses,  
**Genome Res**. 2009. PDF.
11. **Fullwood, M.J.** and Ruan, Y. ChIP-based Methods for the Identification of Long-Range  
Chromatin Interactions,  
**Journal of Cellular Biochemistry**. 2009. PDF.
12. **Fullwood, M.J.;** Tan J. J.; *et al.*  
The Use of Multiple Displacement Amplification to Amplify Complex DNA Libraries,  
**Nucleic Acids Res**. 2008. PDF.
13. Ng, P., Tan; J.J.; Ooi H.S.; Lee Y. L.; Chiu K. P.; **Fullwood M.J., et al.**  
Multiplex Sequencing of Paired End Ditags (MS-PET): A Strategy for the Ultra-High-  
Throughput Analysis of Transcriptomes and Genomes,  
**Nucleic Acids Res**. 2006. PDF.